

Figure 1

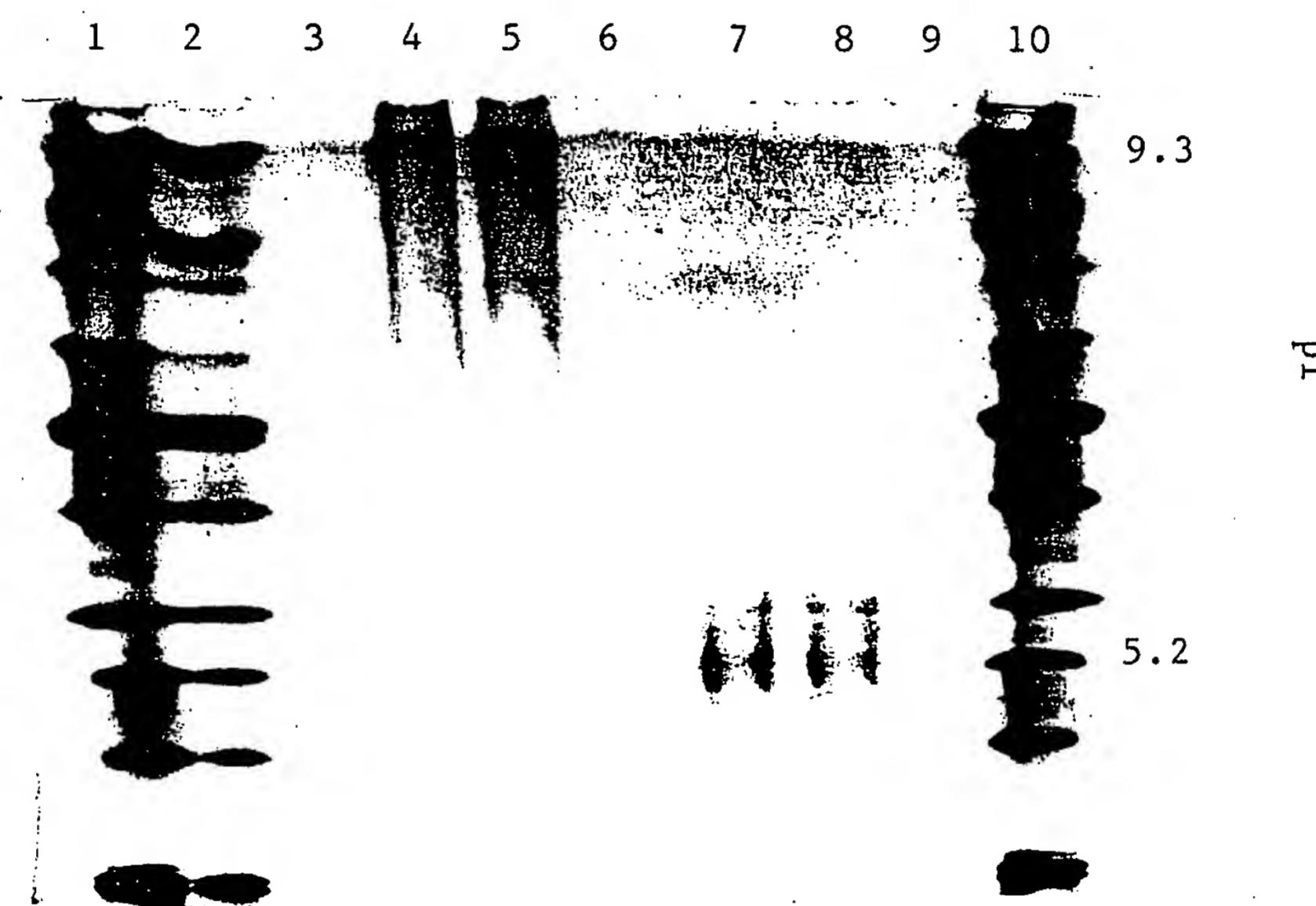


Figure 2

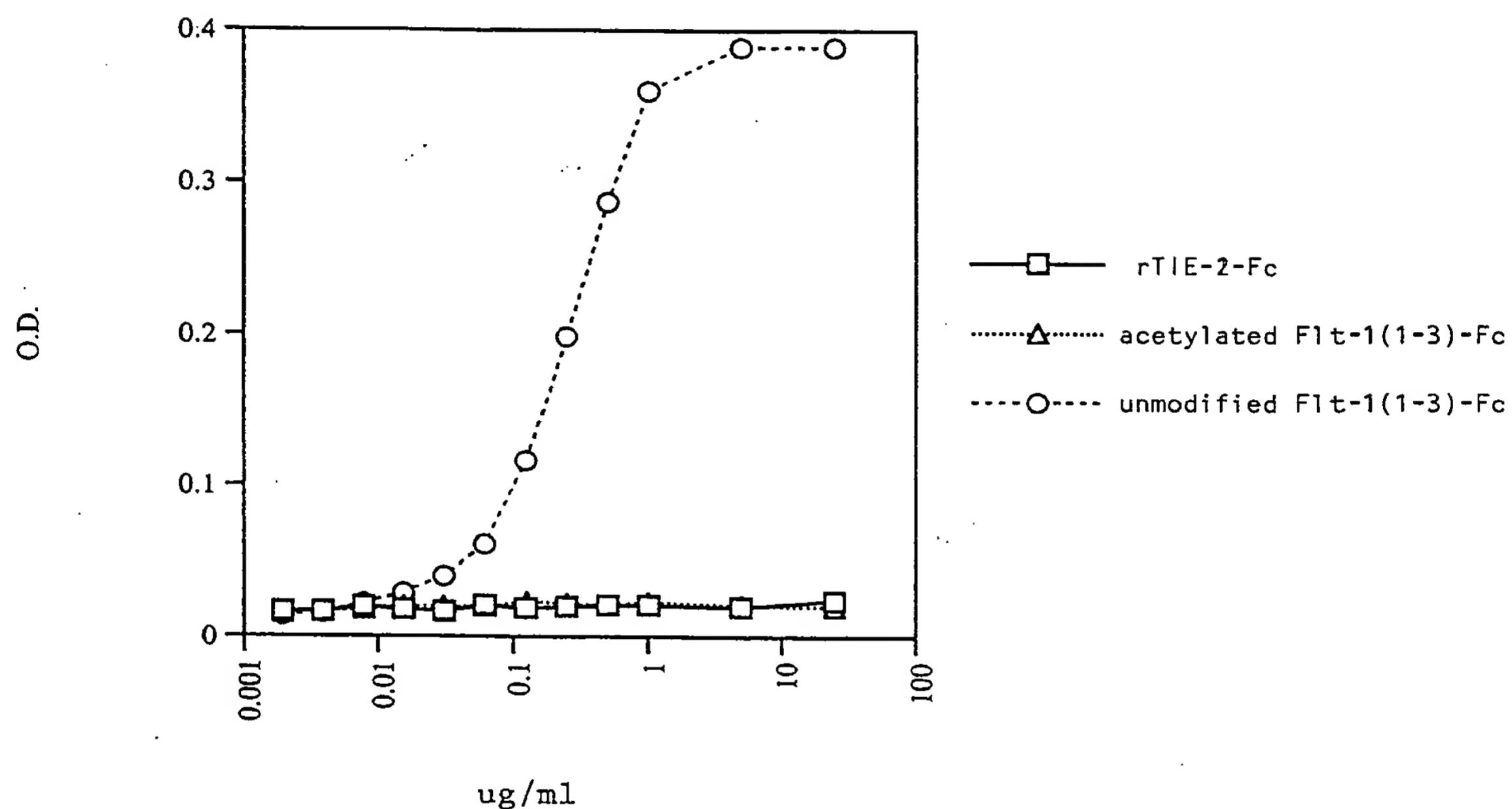


Figure 3

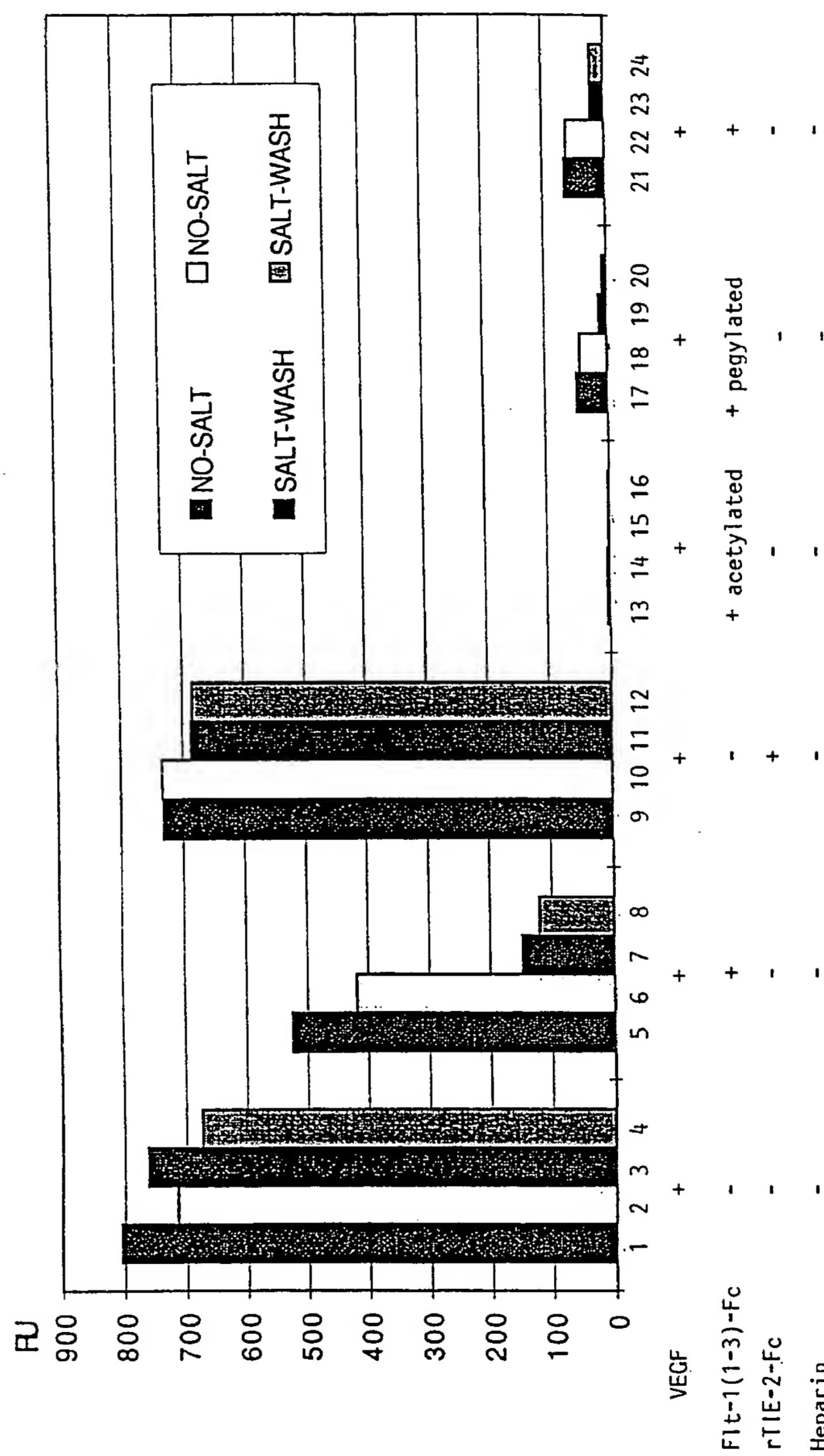


Figure 4

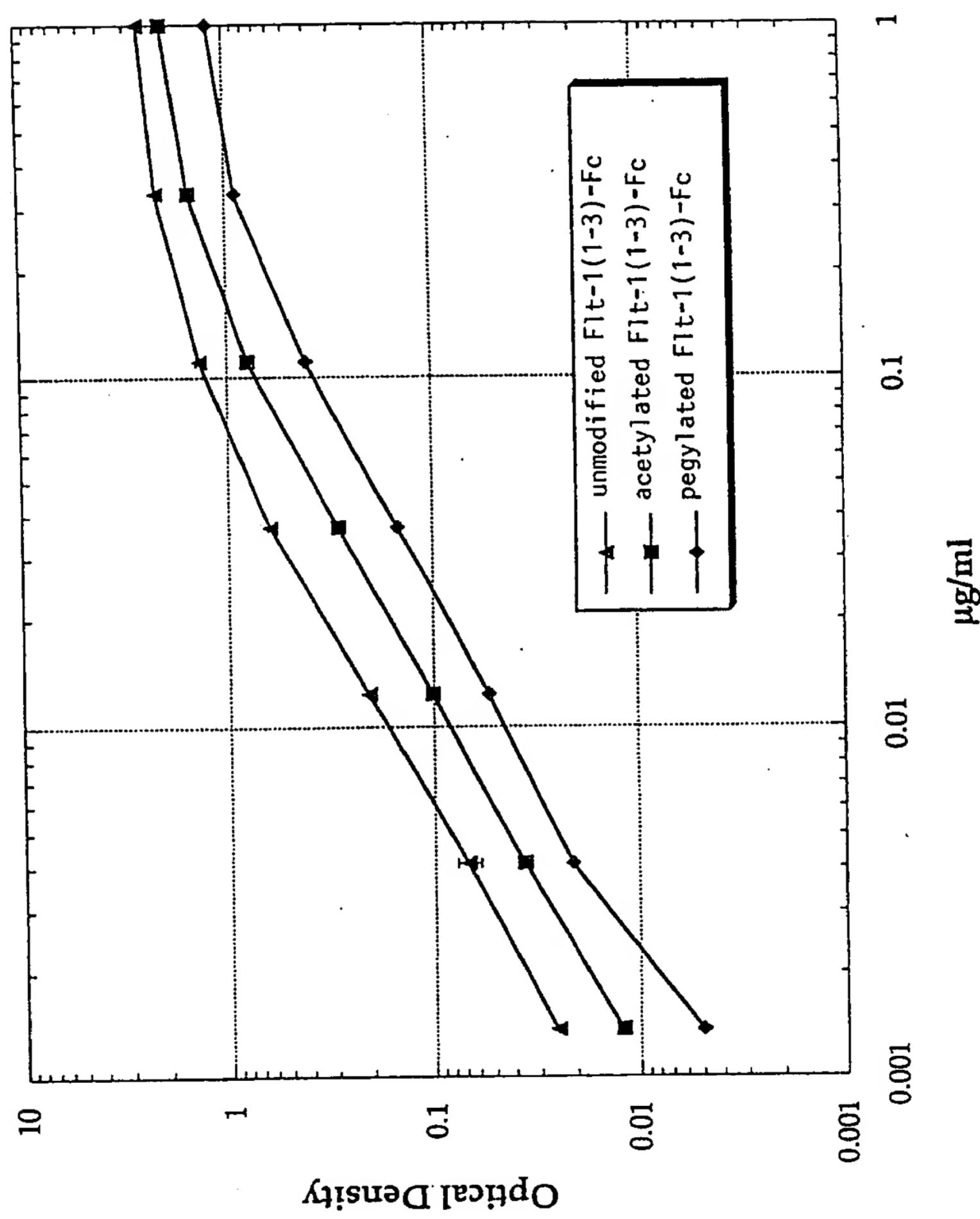


Figure 5

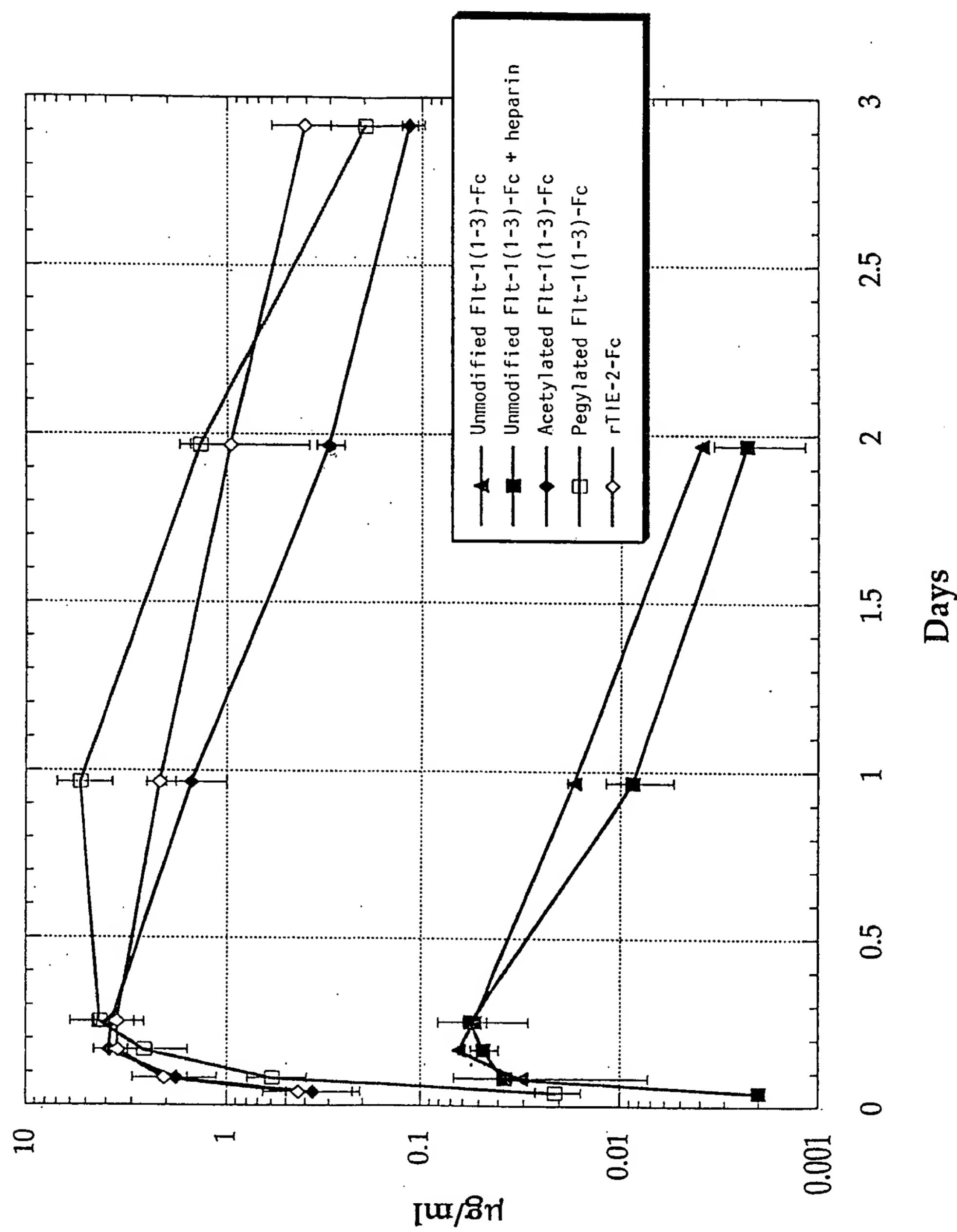


Figure 6A

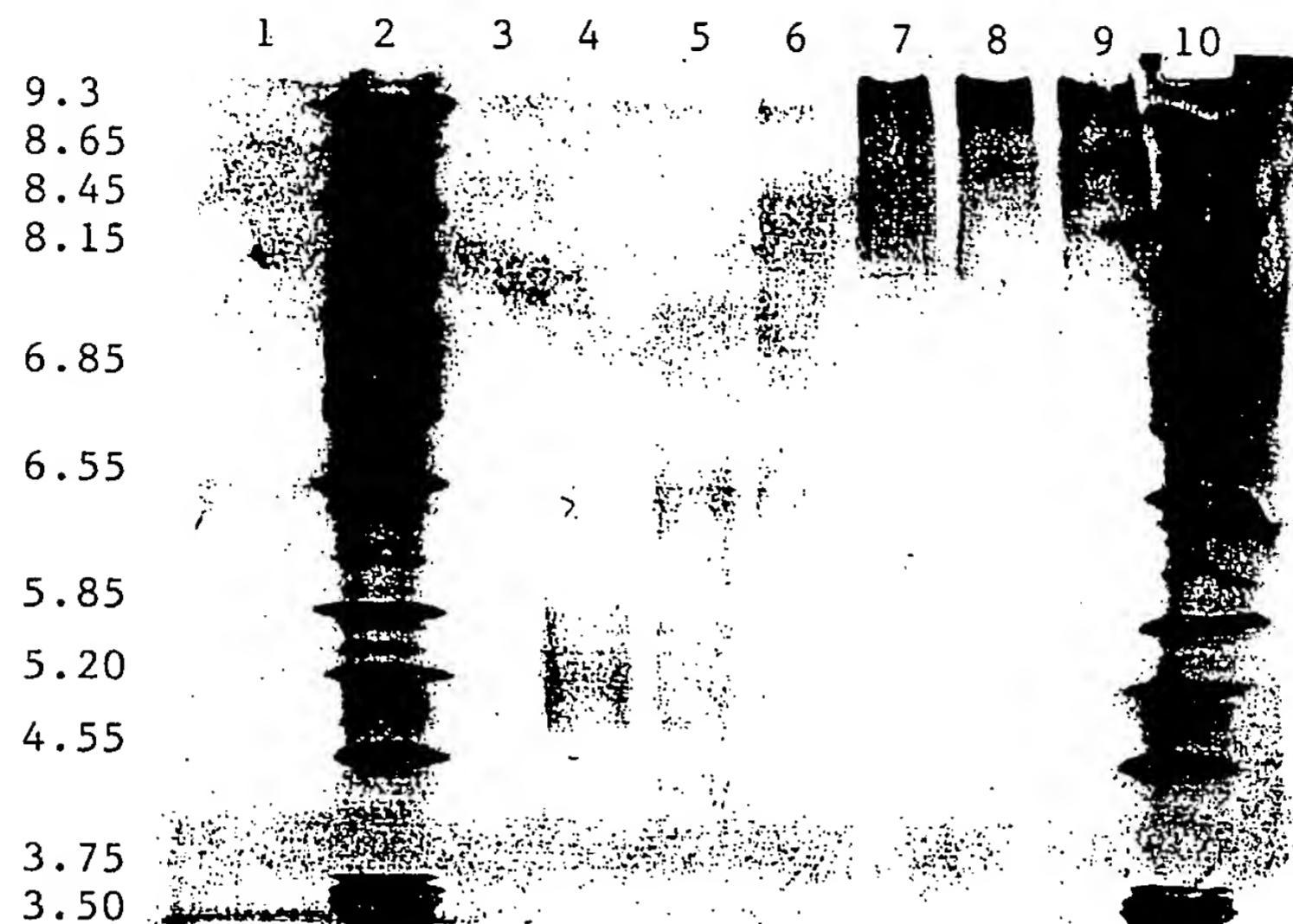


Figure 6B

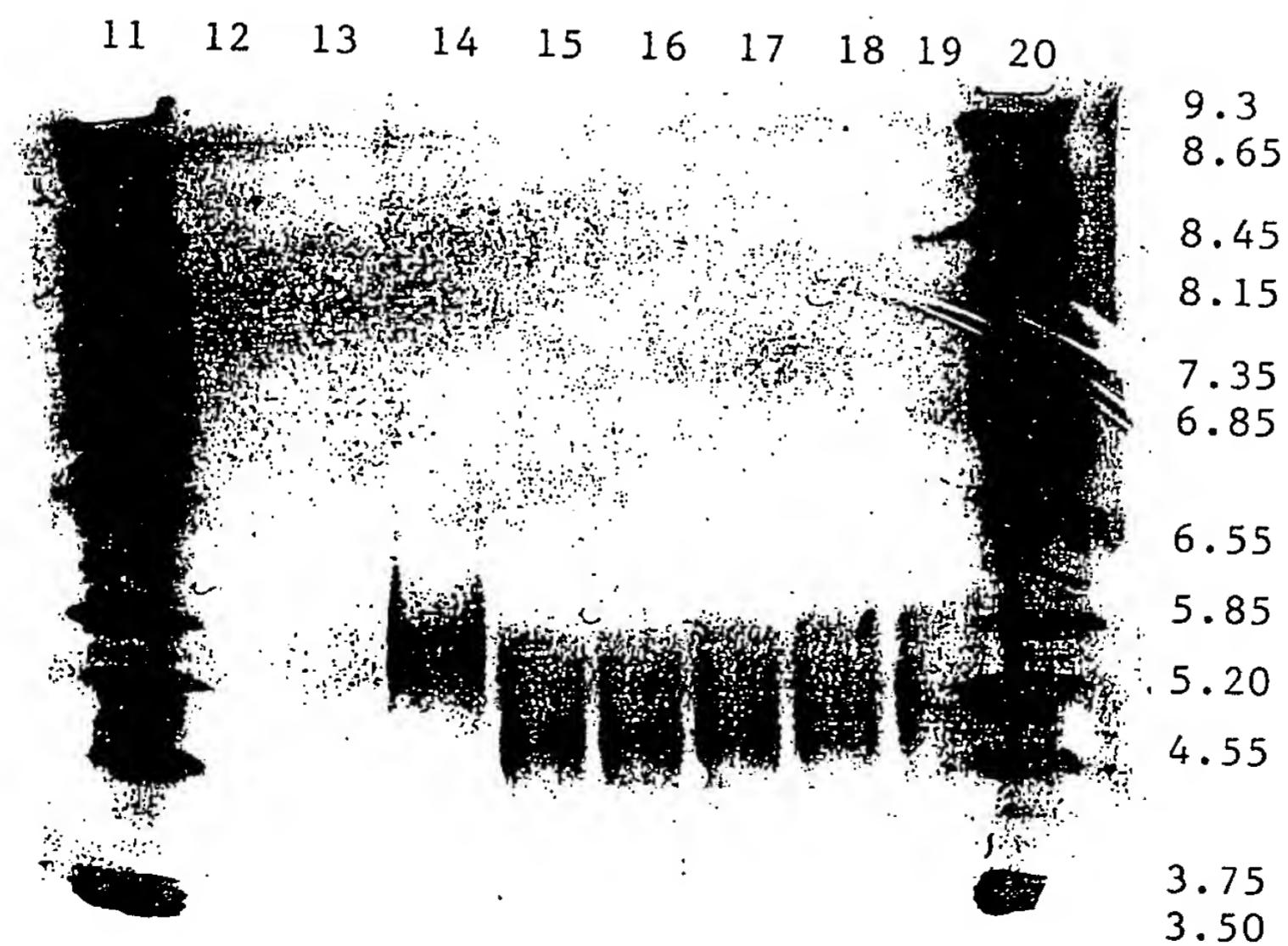


Figure 7

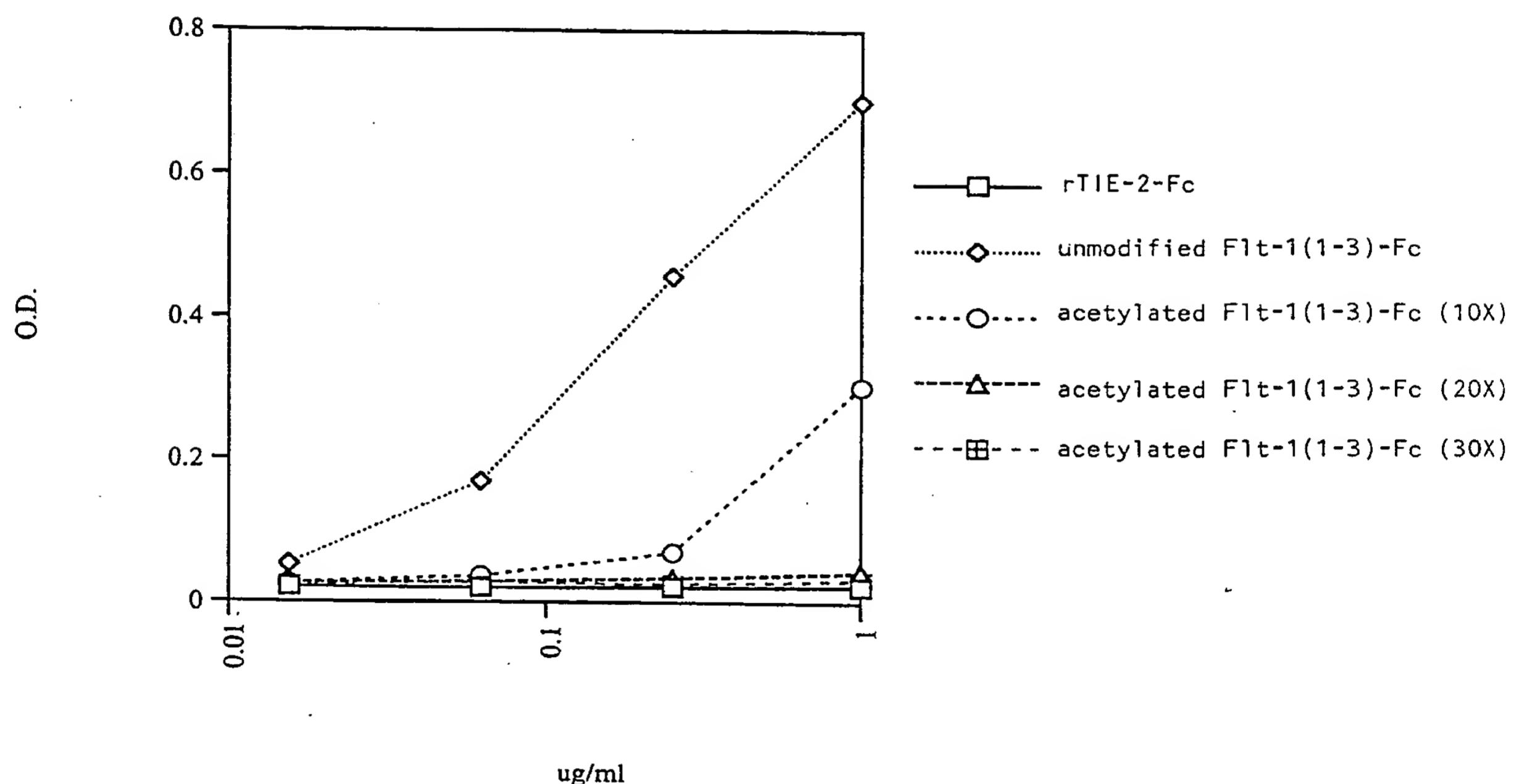
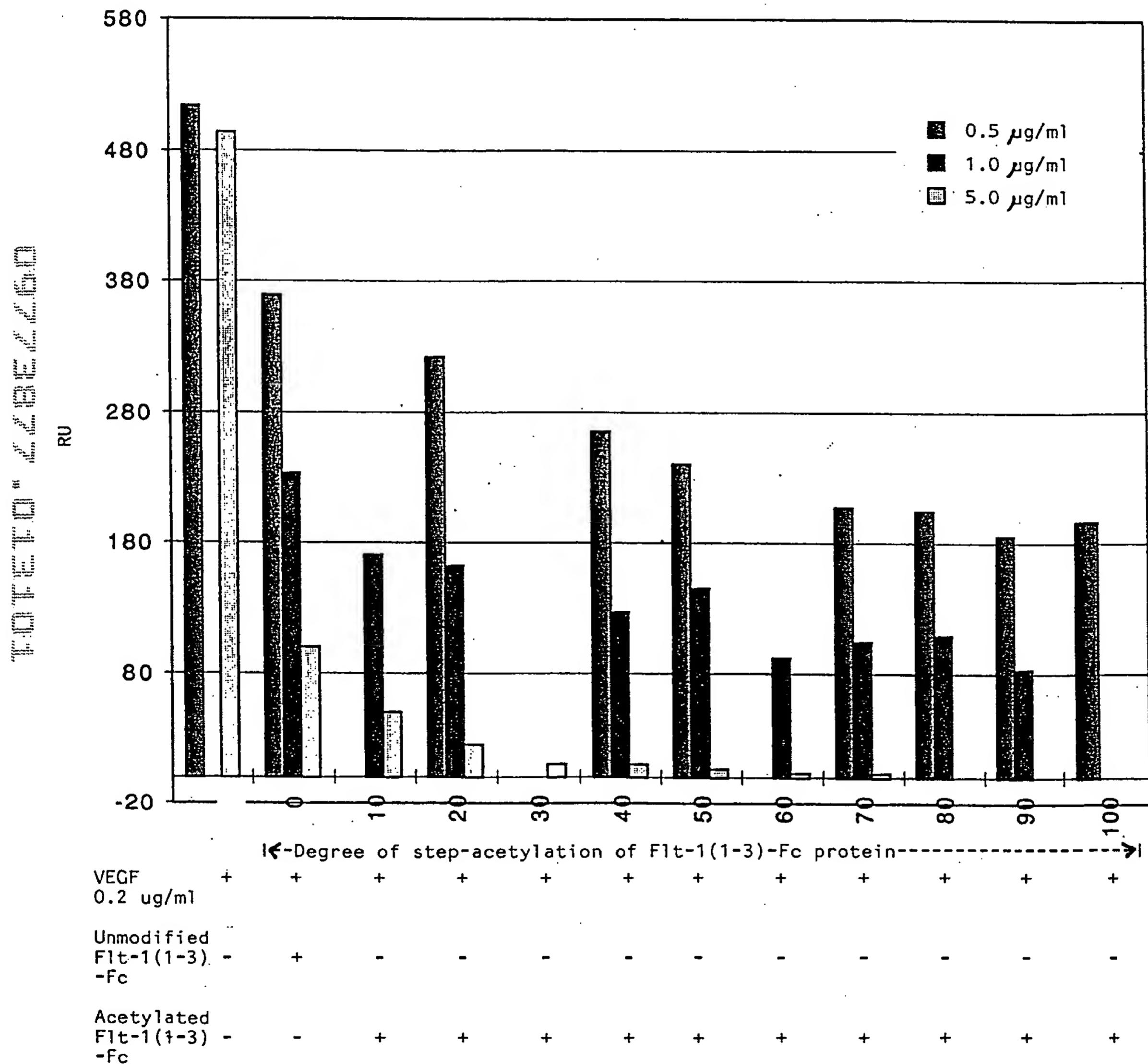


Figure 8



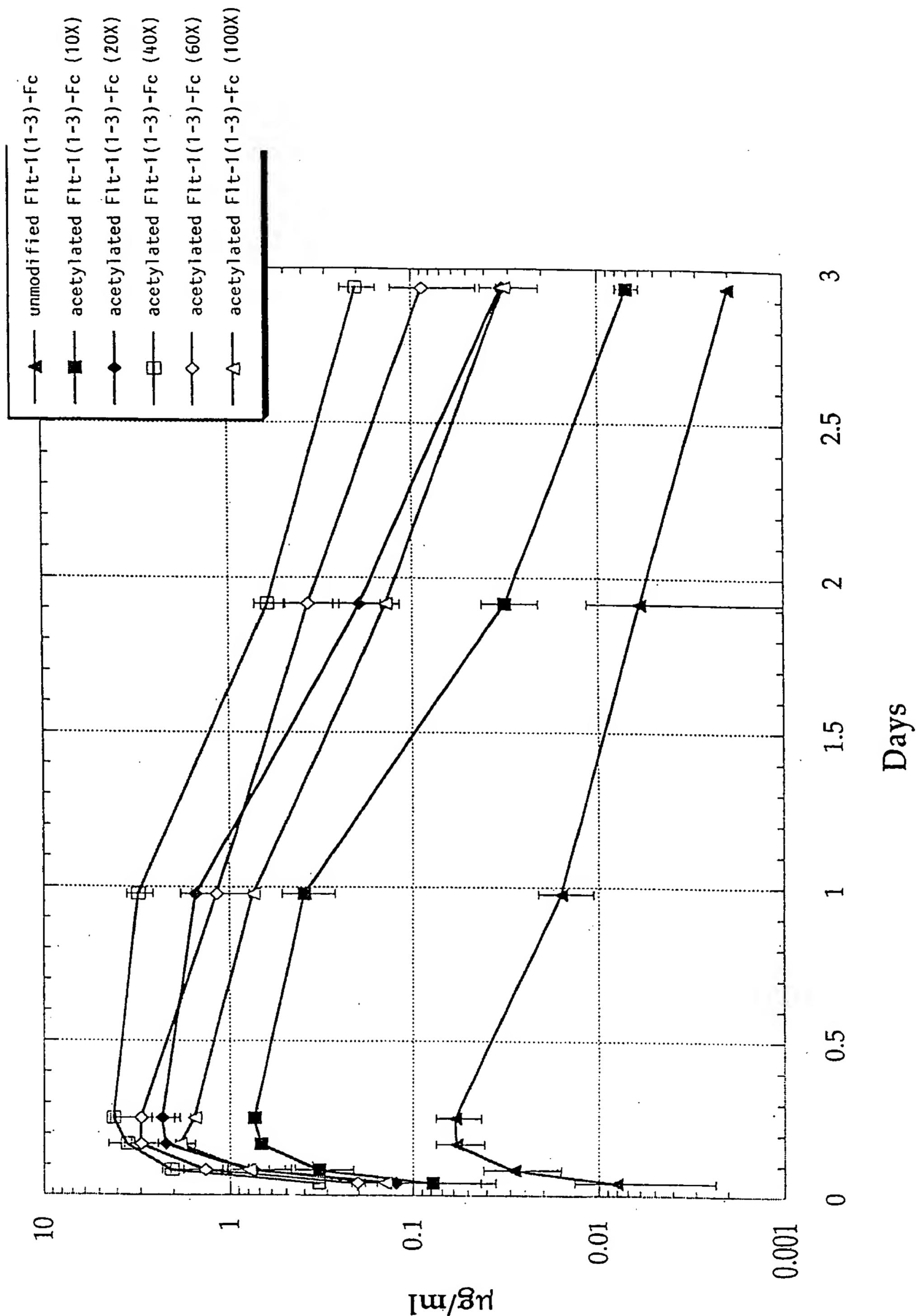


Figure 10A

10	20	30	40	50	60
*	*	*	*	*	*
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu>					
70	80	90	100	110	120
*	*	*	*	*	*
ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC Thr Gly Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>					
130	140	150	160	170	180
*	*	*	*	*	*
CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA GTG TAG TAC GTT CGT CCG GTC TGT GAC GTA GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>					
190	200	210	220	230	240
*	*	*	*	*	*
TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>					
250	260	270	280	290	300
*	*	*	*	*	*
TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>					
310	320	330	340	350	360
*	*	*	*	*	*
CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC CTT TGT His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr>					
370	380	390	400	410	420
*	*	*	*	*	*
GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>					
430	440	450	460	470	480
*	*	*	*	*	*
GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>					
490	500	510	520	530	540
*	*	*	*	*	*
ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>					

Figure 10B

550	560	570	580	590	600
*	*	*	*	*	*
GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>					
610	620	630	640	650	660
*	*	*	*	*	*
GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>					
670	680	690	700	710	720
*	*	*	*	*	*
CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>					
730	740	750	760	770	780
*	*	*	*	*	*
AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>					
790	800	810	820	830	840
*	*	*	*	*	*
AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg>					
850	860	870	880	890	900
*	*	*	*	*	*
CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA GCT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>					
910	920	930	940	950	960
*	*	*	*	*	*
ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>					
970	980	990	1000	1010	1020
*	*	*	*	*	*
TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>					
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Pro Ser Val>					

Figure 10C

1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr>					
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp>					
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr>					
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys>					
1330	1340	1350	1360	1370	1380
*	*	*	*	*	*
TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys>					
1390	1400	1410	1420	1430	1440
*	*	*	*	*	*
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys>					
1450	1460	1470	1480	1490	1500
*	*	*	*	*	*
AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu>					
1510	1520	1530	1540	1550	1560
*	*	*	*	*	*
TGG GAG AGC AAT GGG CAG CGG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser>					
1570	1580	1590	1600	1610	1620
*	*	*	*	*	*
GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly>					

Figure 10D

1630 1640 1650 1660 1670 1680
* * * * * * * *
AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC
TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser>

1690 1700
* * * *
CTC TCC CTG TCT CCG GGT AAA TGA
GAG AGG GAC AGA GGC CCA TTT ACT
Leu Ser Leu Ser Pro Gly Lys ***>

Figure 11

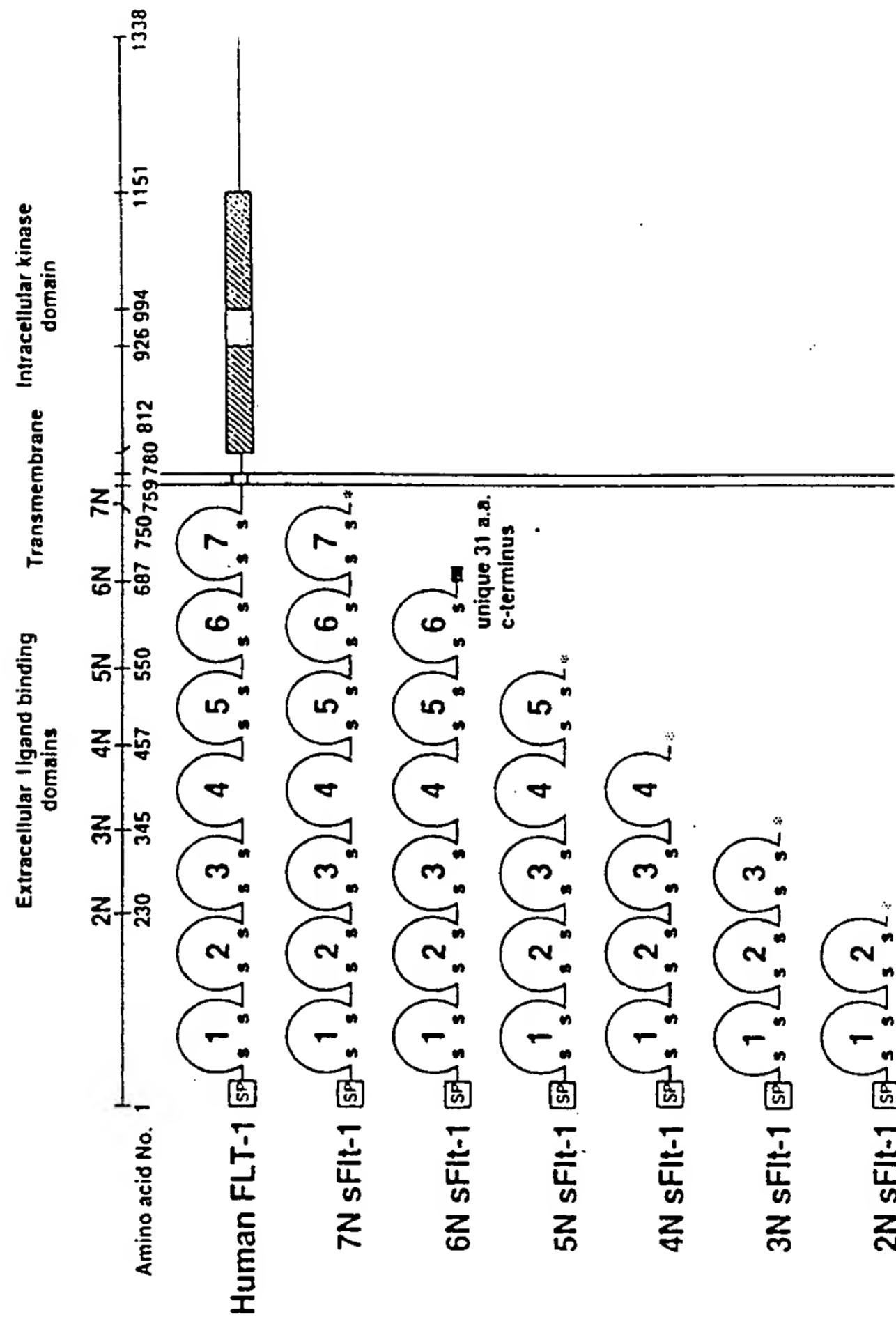


Figure 12A

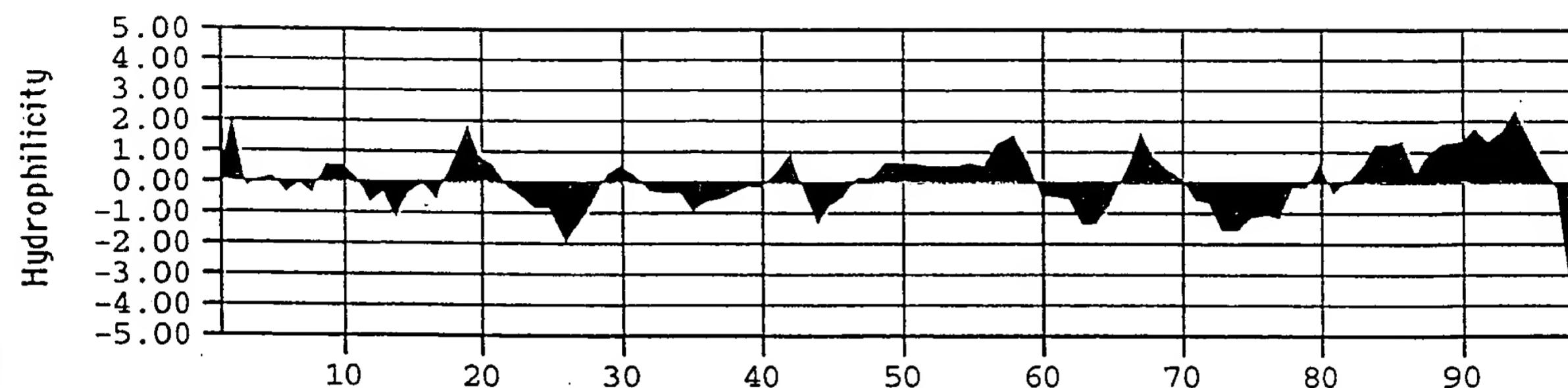


Figure 12B

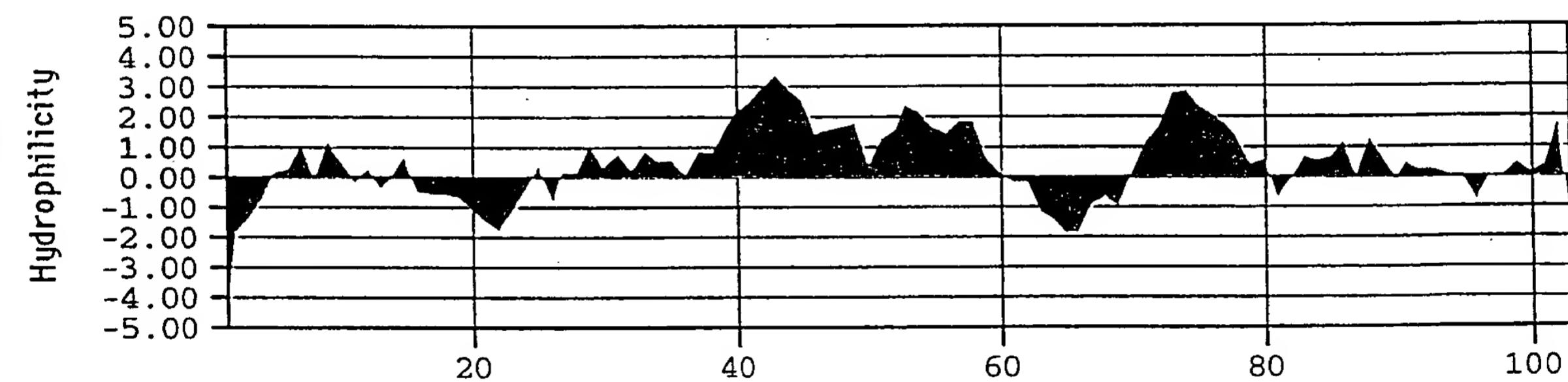


Figure 13A

10	20	30	40	50	60
*	*	*	*	*	*
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>					
70	80	90	100	110	120
*	*	*	*	*	*
ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC Thr Gly Ser Ser Ser Gly Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>					
130	140	150	160	170	180
*	*	*	*	*	*
CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA GTG TAG TAC GTT CGT CCG GTC TGT GAC GTA GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>					
190	200	210	220	230	240
*	*	*	*	*	*
TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>					
250	260	270	280	290	300
*	*	*	*	*	*
TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>					
310	320	330	340	350	360
*	*	*	*	*	*
CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC CTT TGT His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr>					
370	380	390	400	410	420
*	*	*	*	*	*
GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>					
430	440	450	460	470	480
*	*	*	*	*	*
GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>					
490	500	510	520	530	540
*	*	*	*	*	*
ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>					

Figure 13B

550	560	570	580	590	600
*	*	*	*	*	*
GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>					
610	620	630	640	650	660
*	*	*	*	*	*
GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>					
670	680	690	700	710	720
*	*	*	*	*	*
CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>					
730	740	750	760	770	780
*	*	*	*	*	*
AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>					
790	800	810	820	830	840
*	*	*	*	*	*
AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn>					
850	860	870	880	890	900
*	*	*	*	*	*
ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr>					
910	920	930	940	950	960
*	*	*	*	*	*
TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp>					
970	980	990	1000	1010	1020
*	*	*	*	*	*
AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro>					
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG Ala Pro Glu Leu Leu Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Asp Thr>					

Figure 13C

1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp>					
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTC TTA CGG TTC TGT TTC Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys>					
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His>					
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG CAG AGG TTG TTT CGG GAG GGT CGG Gln Asp Trp Leu Asn Gly Lys Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala>					
1330	1340	1350	1360	1370	1380
*	*	*	*	*	*
CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr>					
1390	1400	1410	1420	1430	1440
*	*	*	*	*	*
CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys>					
1450	1460	1470	1480	1490	1500
*	*	*	*	*	*
GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn>					
1510	1520	1530	1540	1550	1560
*	*	*	*	*	*
TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu>					
1570	1580	1590	1600	1610	1620
*	*	*	*	*	*
ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu>					

Figure 13D

1630 1640 1650 1660 1670
* * * * * * *
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>

Figure 14A

10	20	30	40	50	60
*	*	*	*	*	*
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>					
70	80	90	100	110	120
*	*	*	*	*	*
ACA GGA TCT AGT TCC GGA GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC CCC GAA ATT TGT CCT AGA TCA AGG CCT CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG GGG CTT TAA Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile>					
130	140	150	160	170	180
*	*	*	*	*	*
ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA CCT AAC ATC TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT GGA TTG TAG Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile>					
190	200	210	220	230	240
*	*	*	*	*	*
ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA CGC ATA ATC TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT GCG TAT TAG Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile>					
250	260	270	280	290	300
*	*	*	*	*	*
TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA GGG CTT CTG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT CCC GAA GAC Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu>					
310	320	330	340	350	360
*	*	*	*	*	*
ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA CAT CGA CAA TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT GTA GCT GTT Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln>					
370	380	390	400	410	420
*	*	*	*	*	*
ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC AAA TTA CTT AGA GGC TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG TTT AAT GAA TCT CCG Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly>					
430	440	450	460	470	480
*	*	*	*	*	*
CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG AGA GTT CAA ATG ACC GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC TCT CAA GTT TAC TGG His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr>					
490	500	510	520	530	540
*	*	*	*	*	*
TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val>					

Figure 14B

550	560	570	580	590	600
*	*	*	*	*	*
CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GAA TGA TAA CTG TTT TAC GTC TTG CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser>					
610	620	630	640	650	660
*	*	*	*	*	*
GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly>					
670	680	690	700	710	720
*	*	*	*	*	*
GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu>					
730	740	750	760	770	780
*	*	*	*	*	*
GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Asp Thr Leu Met Ile Ser Arg>					
790	800	810	820	830	840
*	*	*	*	*	*
ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC TGG GGA CTC CAG TGT ACG CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe>					
850	860	870	880	890	900
*	*	*	*	*	*
AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG CAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GCA TTA CGG TTC TGT GGC GCC CTC CTC GTC Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln>					
910	920	930	940	950	960
*	*	*	*	*	*
TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn>					
970	980	990	1000	1010	1020
*	*	*	*	*	*
GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr>					
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg>					

Figure 14C

1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC					
CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG					
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser>					
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT					
CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA					
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Thr Thr Pro>					
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC					
GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG					
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser>					
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC					
TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG					
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His>					
1330	1340	1350			
*	*	*	*	*	*
TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA					
ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT					
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>					

Figure 15A

10	20	30	40	50	60
*	*	*	*	*	*
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>					
70	80	90	100	110	120
*	*	*	*	*	*
ACA GGA TCT AGT TCC GGA GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC CCC GAA ATT TGT CCT AGA TCA AGG CCT CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG GGG CTT TAA Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile>					
130	140	150	160	170	180
*	*	*	*	*	*
ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA CCT AAC ATC TAT GTG TAC TGA CTT CCT CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT GGA TTG TAG Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile>					
190	200	210	220	230	240
*	*	*	*	*	*
ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA CGC ATA ATC TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT GCG TAT TAG Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile>					
250	260	270	280	290	300
*	*	*	*	*	*
TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA GGG CTT CTG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT CCC GAA GAC Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu>					
310	320	330	340	350	360
*	*	*	*	*	*
ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA CAT CGA CAA TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT GTA GCT GTT Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln>					
370	380	390	400	410	420
*	*	*	*	*	*
ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC AAA TTA CTT AGA GGC TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG TTT AAT GAA TCT CCG Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly>					
430	440	450	460	470	480
*	*	*	*	*	*
CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG AGA GTT CAA ATG ACC GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC TCT CAA GTT TAC TGG His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr>					
490	500	510	520	530	540
*	*	*	*	*	*
TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA CGA ATT GAC CAA AGC ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT GCT TAA CTG GTT TCG Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser>					

Figure 15B

550	560	570	580	590	600
*	*	*	*	*	*
AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC	TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG	Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp>			
610	620	630	640	650	660
*	*	*	*	*	*
AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA	TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT	Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser>			
670	680	690	700	710	720
*	*	*	*	*	*
GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA	CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT	Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr>			
730	740	750	760	770	780
*	*	*	*	*	*
TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA	ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT	Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro>			
790	800	810	820	830	840
*	*	*	*	*	*
AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC	TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG	Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp>			
850	860	870	880	890	900
*	*	*	*	*	*
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT	CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA	Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His>			
910	920	930	940	950	960
*	*	*	*	*	*
AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC	TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG	Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val>			
970	980	990	1000	1010	1020
*	*	*	*	*	*
CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC	GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG	Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn>			
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA	TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT	Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu>			

Figure 15C

1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG					
GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC					
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu>					
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG					
TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC					
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly>					
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC					
GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG					
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe>					
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC					
GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG					
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys>					
1330	1340	1350	1360	1370	1380
*	*	*	*	*	*
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG					
AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC					
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro>					
*					
GGT AAA TGA					
CCA TTT ACT					
Gly Lys ***>					

Figure 16A

10	20	30	40	50	60
*	*	*	*	*	*
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu>					
70	80	90	100	110	120
*	*	*	*	*	*
ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC Thr Gly Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>					
130	140	150	160	170	180
*	*	*	*	*	*
CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA GTG TAG TAC GTT CGT CCG GTC TGT GAC GTÀ GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>					
190	200	210	220	230	240
*	*	*	*	*	*
TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>					
250	260	270	280	290	300
*	*	*	*	*	*
TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>					
310	320	330	340	350	360
*	*	*	*	*	*
CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC CTT TGT His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr>					
370	380	390	400	410	420
*	*	*	*	*	*
GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>					
430	440	450	460	470	480
*	*	*	*	*	*
GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA Glu Ile Pro Glu Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>					
490	500	510	520	530	540
*	*	*	*	*	*
ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>					

Figure 16B

550	560	570	580	590	600
*	*	*	*	*	*
GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA					
CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT					
Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>					
610	620	630	640	650	660
*	*	*	*	*	*
GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT					
CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA					
Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>					
670	680	690	700	710	720
*	*	*	*	*	*
CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC					
GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG					
Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>					
730	740	750	760	770	780
*	*	*	*	*	*
AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG					
TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC					
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>					
790	800	810	820	830	840
*	*	*	*	*	*
AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AAC GCT TCC GTA AGG CGA					
TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TTG CGA AGG CAT TCC GCT					
Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Asn Ala Ser Val Arg Arg>					
850	860	870	880	890	900
*	*	*	*	*	*
CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA					
GCT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT					
Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>					
910	920	930	940	950	960
*	*	*	*	*	*
ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA					
TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT					
Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>					
970	980	990	1000	1010	1020
*	*	*	*	*	*
TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT					
AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA					
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>					
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC					
CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG					
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val>					

Figure 16C

1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA	AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT	Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr>			
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC	ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG	Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp>			
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CCG GAG GAG CAG TAC AAC AGC ACG TAC	CCG CAC CTC CAC GTA TTA CGG TTC TGT GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG	Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr>			
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG	GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC	Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys>			
1330	1340	1350	1360	1370	1380
*	*	*	*	*	*
TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA	ACG TTC CAG AGG TTG TTT CCG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT	Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys>			
1390	1400	1410	1420	1430	1440
*	*	*	*	*	*
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG	CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC	Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys>			
1450	1460	1470	1480	1490	1500
*	*	*	*	*	*
AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG	TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC	Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu>			
1510	1520	1530	1540	1550	1560
*	*	*	*	*	*
TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC	ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG	Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser>			
1570	1580	1590	1600	1610	1620
*	*	*	*	*	*
GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG	CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC	Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly>			

Figure 16D

1630	1640	1650	1660	1670	1680
*	*	*	*	*	*
AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC					
TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG					
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser>					
1690	1700				
*	*	*	*		
CTC TCC CTG TCT CCG GGT AAA TGA					
GAG AGG GAC AGA GGC CCA TTT ACT					
Leu Ser Leu Ser Pro Gly Lys ***>					

Figure 17

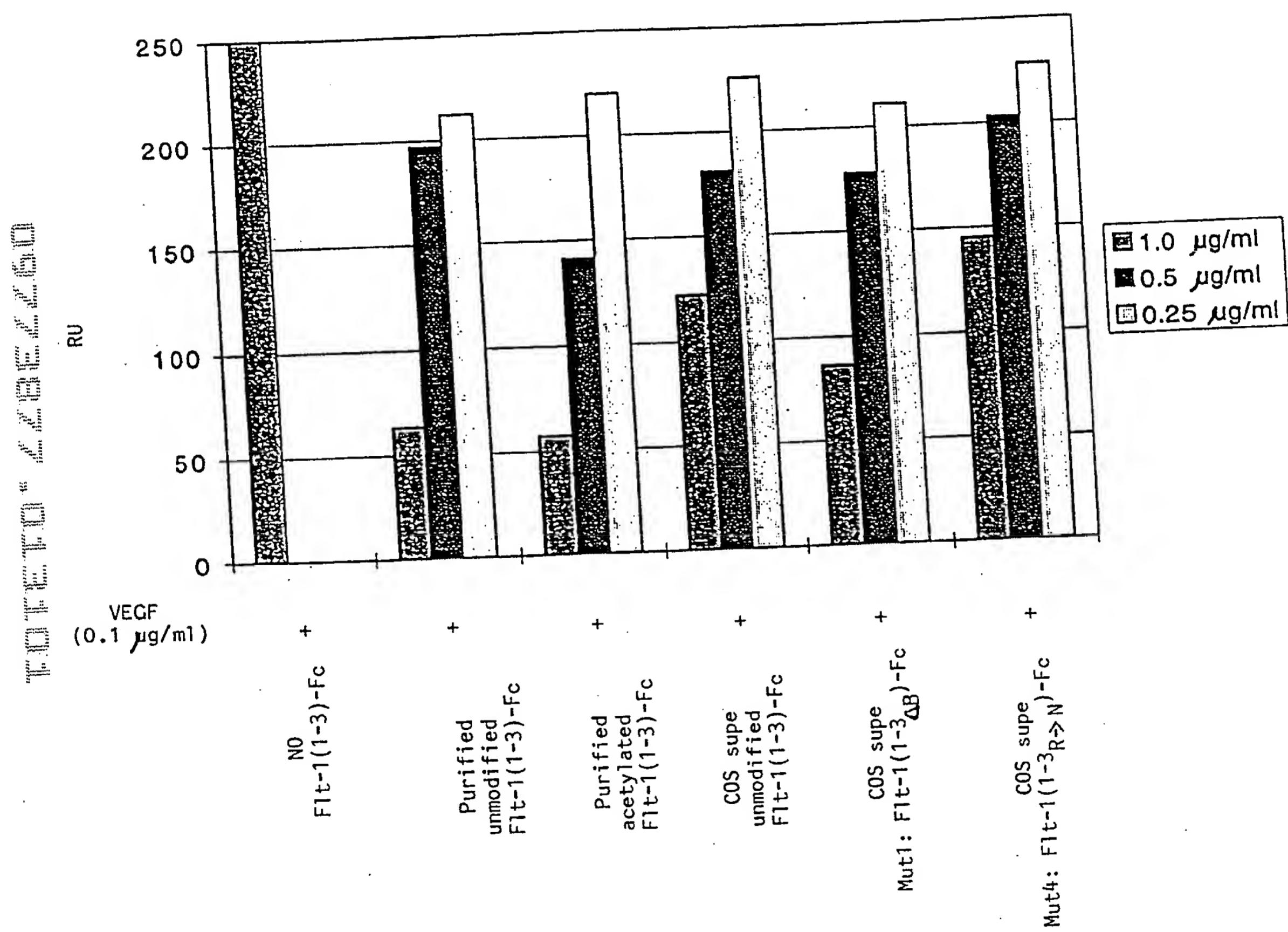


Figure 18

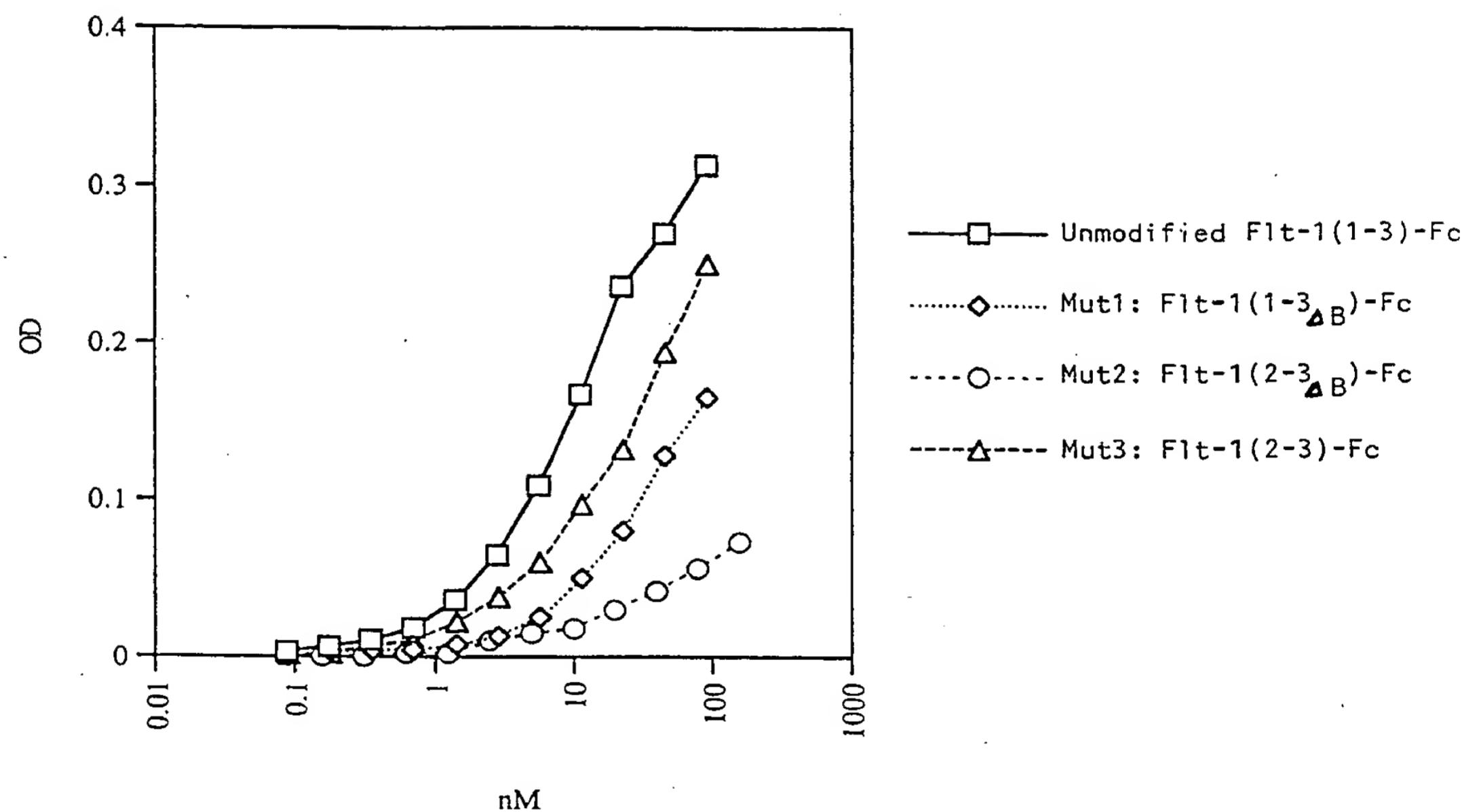


Figure 19

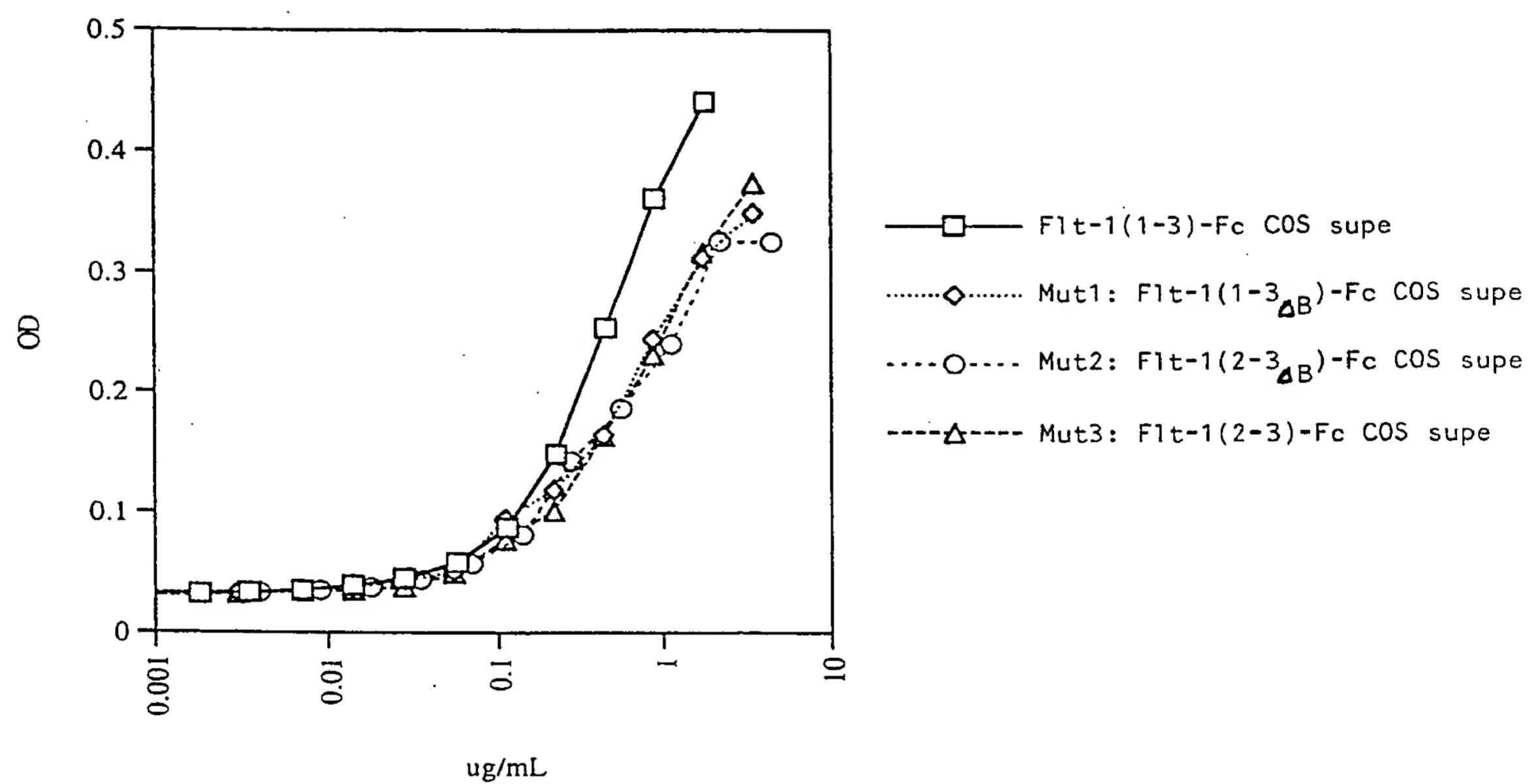


Figure 20

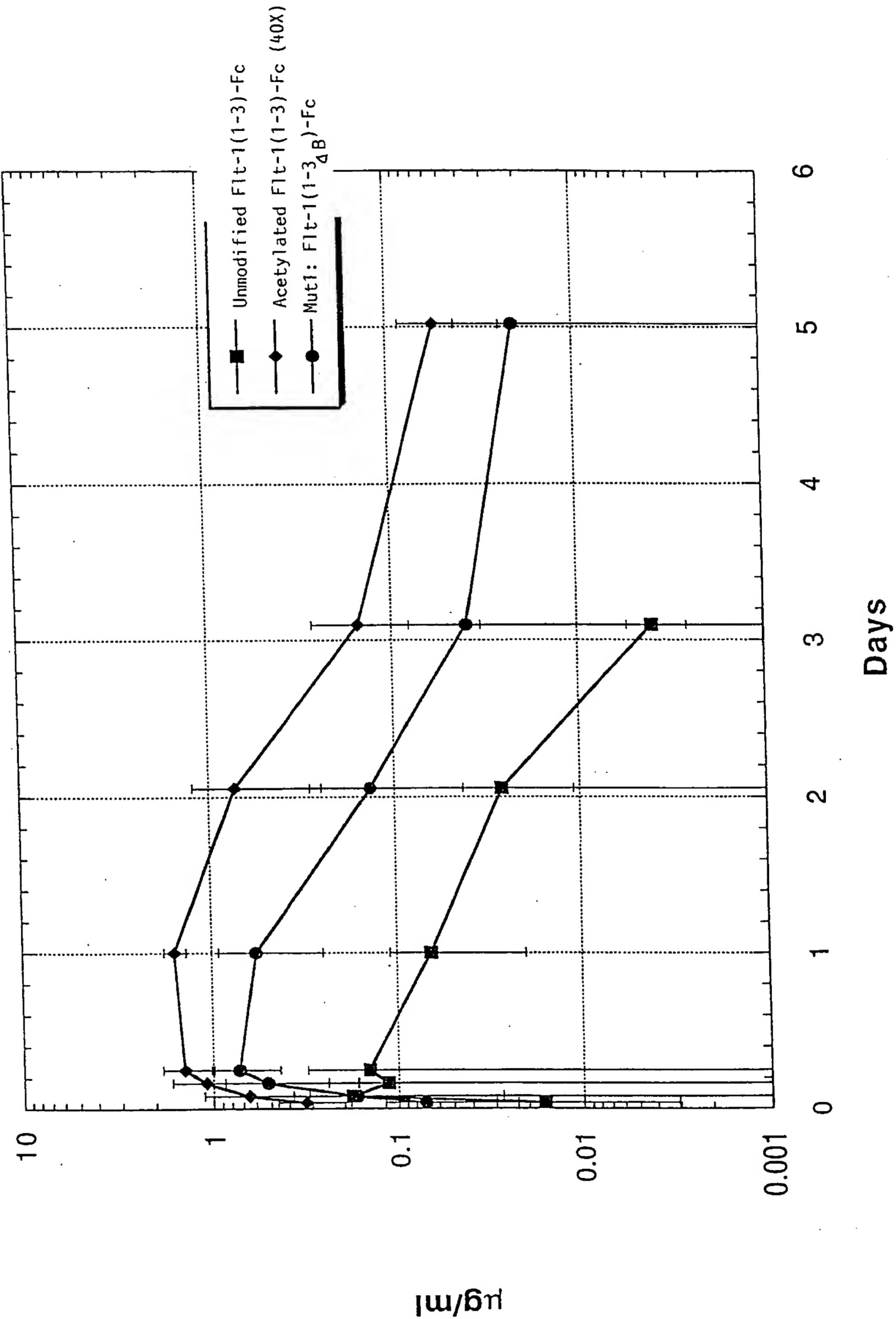


Figure 21A

>EcoRI_site

10	20	30	40	50	60	70	80
AAGCTTGGGCTGCAGGTGATCGACTCTAGAGGATCGATCCCCGGCGAGCTCGAATTGCAACCACCATGGTCAGCTAC							
TTCGAACCCGACGTCCAGCTAGCTGAGATCTCCTAGCTAGGGGCCGCTGAGCTTAAGCGTTGGTGGTACCAAGTCGATG							
M V S Y>							
1 4							

>BspEI_bridge

90	100	110	120	130	140	150	160
TGGGACACCGGGGTCCCTGCTGTGCGCGCTGCTCAGCTGTCGCTTCACAGGATCTAGTTCCGGAGGTAGACCTTCGT							
ACCCTGTGGCCCCAGGACGACACGCGCGACGAGTCGACAGACGAAGAGTGTCTAGATCAAGGCCTCCATCTGGAAAGCA							
W D T G V L L C A L L S C L L L T G S S>							
<u>FLT1 SS</u> >							
S G>							

170	180	190	200	210	220	230	240
AGAGATGTACAGTGAAATCCCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTAC							
TCTCTACATGTCACTTTAGGGCTTAATATGTGTACTGACTTCCTCCCTCGAGCAGTAAGGGACGGCCCAATGCAGTG							
E M Y S E I P E I I H M T E G R E L V I P C R V T S>							
57.							
<u>HFLT1 D2</u> >							

250	260	270	280	290	300	310	320
CTAACATCACTGTTACTTAAAAAGTTCCACTTGACACTTGATCCCTGATGGAAAACGCATAATCTGGGACAGTAGA							
GATTGTAGTGACAATGAAATTTCCTCAAAGGTGAAGTGTGAAACTAGGGACTACCTTTGCGTATTAGACCCCTGTCATCT							
P N I T V T L K K F P L D T L I P D G K R I I W D S R>							
84.							
<u>HFLT1 D2</u> >							

330	340	350	360	370	380	390	400
AAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTCTGACCTGTGAAGCAACAGTCATGGCATTGTA							
TTCCCGAAGTAGTATAGTTACGTTGCATGTTCTTATCCCAGAAGACTGGACACTTCGTTGTCAGTTACCGTAAACAT							
K G F I I S N A T Y K E I G L L T C E A T V N G H L Y>							
111.							
<u>HFLT1 D2</u> >							

410	420	430	440	450	460	470	480
TAAGACAAACTATCTCACACATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCTCGTCATGGAATTGAACAT							
ATTCTGTTGATAGAGTGTAGCTGTTGGTTATGTTAGTATCTACACCAAGACTCAGGGCAGAGTACCTTAACCTGATA							
K T N Y L T H R Q T N T I I D>							
<u>HFLT1 D2</u> >							
V V L S P S H G I E L>							
137.							
<u>HFLK1 D3</u> >							

Figure 21B

490 500 510 520 530 540 550 560

CTGTTGGAGAAAAGCTTGTCTAAATTGTACAGCAAGAACACTGAACATAAATGTGGGATTGACTTCACACTGGGAATACCCCT
GACAACCTCTTCGAACAGAATTAAACATGTCGTTCTGACTTGATTTACACCCCTAACTGAAGTTGACCCTATGGGA
S V G E K L V L N C T A R T E L N V G I D F N W E Y P>
164
HFLK1 D3 >

570 580 590 600 610 620 630 640

TCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTGGAG
AGAAGCTTCGTAGTCGTATTCTTGAACATTGGCTCTGGATTTGGTCAGACCCCTCACTCTACTTCTTAAAAACTC
S S K H Q H K K L V N R D L K T Q S G S E M K K F L S>
191
HFLK1 D3 >

650 660 670 680 690 700 710 720

CACCTTAACTATAGATGGTGTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGCTGATGACCAAGA
GTGGAATTGATATCTACCACATTGGCCTCACTGGTCCTAACATGTGGACACGTCGTAGGTACCCGACTACTGGTTCT
T L T I D G V T R S D Q G L Y T C A A S S G L M T K>
217
HFLK1 D3 >

>Srf_Bridge_

730 740 750 760 770 780 790 800

AGAACAGCACATTGTCAGGGTCCATGAAAAGGGCCGGCGACAAAACCTCACACATGCCACCCTGCCCCAGCACCTGAA
TCTTGTGTTAAACAGTCCCAGGTACTTTCCCGGGCCCGTGTGAGTGTACGGGTGGCACGGGTGACTGGTGGACTT
K N S T F V R V H E K>
HFLK1 D3 >
G P G >
D K T H T C P P C P A P E>
244
FCΔC1 (A) >

810 820 830 840 850 860 870 880

CTCCTGGGGGACCGTCAGTCTCCTCTCCCCCAAAACCCAAGGACACCCTCATGATCTCCGGACCCCTGAGGTAC
GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTGGGTCCTGTGGAGTACTAGAGGGCTGGGACTCCAGTG
L L G G P S V F L F P P K P K D T L M I S R T P E V T>
271
FCΔC1 (A) >

890 900 910 920 930 940 950 960

ATGCGTGGTGGACGTGAGCCACGAAGAACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
TACGCACCACCACTGCACTCGGTGCTCTGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
C V V V D V S H E D P E V K F N W Y V D G V E V H N>
297
FCΔC1 (A) >

970 980 990 1000 1010 1020 1030 1040

CCAAGACAAAGCCGCGGGAGGAGCAGTACAACACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAAGGACTGG
GGTTCTGTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC
A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W>
324
FCΔC1 (A) >

Figure 21C

1050 1060 1070 1080 1090 1100 1110 1120
 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAA
 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTGGGGAGGGTAGCTCTTGGTAGAGGTTCGGTT
 L N G K E Y K C K V S N K A L P A P I E K T I S K A R>
 351
 FCΔC1 (A) >

>A>C_A_allotype
 |
 >G>T_A_allotype
 | |
 1130 1140 1150 1160 1170 1180 1190 1200
 AGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCATCCCGGATGAGCTGACCAAGAACCAAGGTCAGCCTGACCT
 TCCCGTCGGGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTCTGGTCCAGTCGGACTGGA
 G Q P R E P Q V Y T L P P S R D E L T K N Q V S L T>
 377
 FCΔC1 (A) >

1210 1220 1230 1240 1250 1260 1270 1280
 GCCTGGTCAAAGGTTCTATCCCAGCGACATGCCGTGGAGTGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC
 CGGACCAAGTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCCTCGTTACCGTCGGCTCTGGTGTGATGTTCTGG
 C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T>
 404
 FCΔC1 (A) >

>T>C
 |
 1290 1300 1310 1320 1330 1340 1350 1360
 ACGCCTCCCGTGCTGGACTCCGACGGCTCTTCTTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG
 TGGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATATCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC
 T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G>
 431
 FCΔC1 (A) >

1370 1380 1390 1400 1410 1420 1430 1440
 GAACGTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
 CTTGCAGAAGAGTACGAGGCACCTACGTACTCCGAGACGTGGTGTGATGTGCGTCTCGGAGAGGGACAGAGGCCCAT
 N V F S C S V M H E A L H N H Y T Q K S L S L S P G>
 457
 FCΔC1 (A) >

>NotI_site
 |
 | 1450
 AATGAGCGGCCGC
 TTACTCGCCGGCG
 K *>
 458
 >

Figure 22A

>EcoRI_site

10	20	30	40	50	60	70	80
AAGCTTGGGCTGCAGGTCGATCGACTCTAGAGGATCGATCCCCGGCGAGCTCGAACCAACCACCATGGTCAGCTAC							
TTCGAACCCGACGTCCAGCTAGCTGAGATCTCCTAGCTAGGGGCCGCTCGAGCTTAAGCGTTGGTAGGCTACAGTCGATG							
M V S Y>							
1 4							
>							

>BspEI_bridge

90	100	110	120	130	140	150	160
TGGGACACCGGGGCTGCTGTGCGCGCTGCTCAGCTGTCTCACAGGATCTAGTTCCGGAGGTAGACCTTCGT							
ACCCGTGGCCCCAGGACGACACGCGCGACGAGTCGACAGACGAAGAGTGTCTAGATCAAGGCCTCCATCTGGAAAGCA							
W D T G V L L C A L L S C L L L T G S S>							
FLT1 SIGNAL SEQUENCE							
S G>							
G R P F V>							
31							
>							

170 180 190 200 210 220 230 240

AGAGATGTACAGTGAAATCCCCGAAATTATAACACATGACTGAAGGAAGGGAGCTCGTATTCCCTGCCGGTTACGTAC							
TCTCTACATGTCACTTAGGGCTTAATATGTGTACTGACTTCCTCCCTCGAGCAGTAAGGGACGGCCAATGCAGTG							
E M Y S E I P E I I H M T E G R E L V I P C R V T S>							
57							
FLT1 IG DOMAIN 2							

250 260 270 280 290 300 310 320

CTAACATCACTGTTACTTTAAAAAGTTCCACTTGACACTTGATCCCTGATGGAAAACGCATAATCTGGGACAGTAGA							
GATTGTAGTGACAATGAAATTTTCAAAGGTGAAGTGTGAAACTAGGGACTACCTTTGCGTATTAGACCCCTGTCATCT							
P N I T V T L K K F P L D T L I P D G K R I I W D S R>							
84							
FLT1 IG DOMAIN 2							

330 340 350 360 370 380 390 400

AAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTCTGACCTGTGAAGCAACAGTCAAATGGGCATTGTA							
TTCCCGAAGTAGTATAGTTACGTTGCATGTTCTTATCCGAAGACTGGACACTCGTTGTCAGTTACCGTAAACAT							
K G F I I S N A T Y K E I G L L T C E A T V N G H L Y>							
111							
FLT1 IG DOMAIN 2							

410 420 430 440 450 460 470 480

TAAGACAAACTATCTCACACATCGACAAACCAATAACATAGATATCCAGCTGTGCCCAGGAAGTCGCTGGAGCTGC							
ATTCTGTTGATAGAGTGTAGCTGTTGGTTATGTTAGTATCTAGGTGACAAACGGGTCTTCAGCGACCTCGACG							
K T N Y L T H R Q T N T I I D>							
FLT1 IG DOMAIN 2							
I Q L L P R K S L E L>							
137							
VEGFR3 (FLT4) IG DOMAIN 3							

Figure 22B

490 500 510 520 530 540 550 560

TGGTAGGGAGAAGCTGGCCTCAACTGCACCGTGTGGCTGAGTTAACACTCAGGTGTACCTTGACTGGGACTACCCA
 ACCATCCCCTCTCGACCAGGAGTTGACGTGGCACACCCGACTCAAATTGAGTCCACAGTGGAAACTGACCCCTGATGGGT
 L V G E K L V L N C T V W A E F N S G V T F D W D Y P >
 164

VEGFR3 (FLT4) IG DOMAIN 3 >

570 580 590 600 610 620 630 640

GGGAAGCAGGCAGAGCGGGGTAAGTGGGTGCCGAGCGACGCTCCAAACAGACCCACACAGAACTCTCCAGCATCCTGAC
 CCCTTCGTCCGTCTCGCCCCATTCAACCCACGGGCTCGCTCGAGGGTTGTCTGGGTGTCTGAGAGGTCGTAGGACTG
 G K Q A E R G K W V P E R R S Q Q T H T E L S S I L T >
 191

VEGFR3 (FLT4) IG DOMAIN 3 >

650 660 670 680 690 700 710 720

CATCCACAACGTCAGCCAGCACGACCTGGCTCGTATGTGTGCAAGGCCAACACGGCATCCAGCGATTTCGGGAGAGCA
 GTAGGTGTTGCAGTCGGTCGTGGACCCGAGCATAACACACGTTCCGGTTGTGCGTAGGTCGCTAAAGCCCTCTCGT
 I H N V S Q H D L G S Y V C K A N N G I Q R F R E S >
 217

VEGFR3 (FLT4) IG DOMAIN 3 >

730 740 750 760 770 780 790 800

CCGAGGTCATGTGCATGAAAATGGCCGGGCGACAAAACACTCACACATGCCAACCGTGCCCCAGCACCTGAACCTGCGGG
 GGCTCCAGTAACACGTACTTTACCGGGCCCGCTGTTTGAGTGTACGGGTGGCACGGTCGTGGACTTGAGGACCCC
 T E V I V H E N >

VEGFR3 (FLT4) IG >

G P G >

D K T H T C P P C P A P E L L G >
 244

FCΔC1 - A ALLOTYPE >

810 820 830 840 850 860 870 880

GGACCGTCAGTCCTCCCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCGGACCCCTGAGGTCACATGCGTGGT
 CCTGGCAGTCAGAAGGAGAAGGGGGTTTGGGTCTGTGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGCACCA
 G P S V F L F P P K P K D T L M I S R T P E V T C V V >
 271

FCΔC1 - A ALLOTYPE >

890 900 910 920 930 940 950 960

GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA
 CCACCTGCACTCGGTGCTCTGGACTCCAGTTCAAGTTGACCATGCACCTGCCACCTCACGTATTACGGTTCTGTT
 V D V S H E D P E V K F N W Y V D G V E V H N A K T >
 297

FCΔC1 - A ALLOTYPE >

970 980 990 1000 1010 1020 1030 1040

AGCCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGAATGGC
 TCGGCGCCCTCCTCGTCATGTTGCGATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGCTGACCGACTTACCG
 K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G >
 324

FCΔC1 - A ALLOTYPE >

Figure 22C

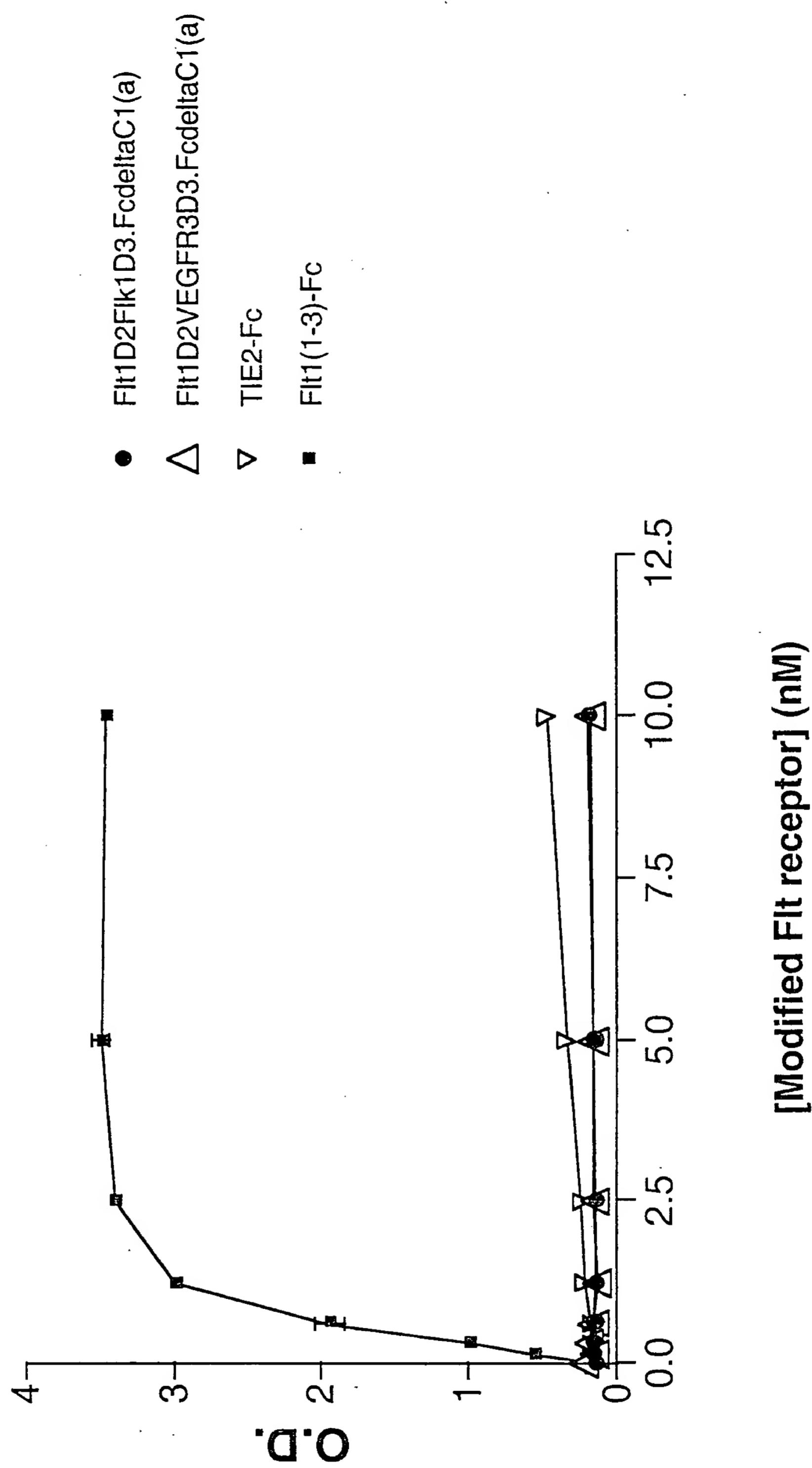
Figure 23

Figure 24A

10 20 30 40 50 60
 * * * * * *
 ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
 TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC CGC GAC GAG TCG ACA GAC GAA GAG
 M V S Y W D T G V L L C A L L S C L L L>
 1 5 hFLT1 SIGNAL SEQUENCE 15 20>

70 80 90 100 110 120
 * * * * * *
 ACA GGA TCT AGT TCC GGA AGT GAT ACC GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC
 TGT CCT AGA TCA AGG CCT TCA CTA TGG CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG
 T G S S S G>
 21_hFLT1 SIGNAL SEQ_26>
 S D T G R P F V E M Y S E I>
 27 30 hFLT1 IG DOMAIN 2 40>

130 140 150 160 170 180
 * * * * * *
 CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA
 GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT
 P E I I H M T E G R E L V I P C R V T S>
 41 45 hFLT1 IG DOMAIN 2 55 60>

190 200 210 220 230 240
 * * * * * *
 CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA
 GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT
 P N I T V T L K K F P L D T L I P D G K>
 61 65 hFLT1 IG DOMAIN 2 75 80>

250 260 270 280 290 300
 * * * * * *
 CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA
 GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT
 R I I W D S R K G F I I S N A T Y K E I>
 81 85 hFLT1 IG DOMAIN 2 95 100>

310 320 330 340 350 360
 * * * * * *
 GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA
 CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTC AAC ATA TTC TGT TTG ATA GAG TGT
 G L L T C E A T V N G H L Y K T N Y L T>
 101 105 hFLT1 IG DOMAIN 2 115 120>

370 380 390 400 410 420
 * * * * * *
 CAT CGA CAA ACC AAT ACA ATC ATA GAT GTG GTT CTG AGT CCG TCT CAT GGA ATT GAA CTA
 GTA GCT GTT TGG TTA TGT TAG TAT CTA CAC CAA GAC TCA GGC AGA GTC CCT TAA CTT GAT
 H R Q T N T I I D>
 121 hFLT1 IG DOMAIN 2 129>
 V V L S P S H G I E L>
 130 hFLT1 IG DOMAIN 3 140>

Figure 24B

430 440 450 460 470 480
 * * * * * *

TCT GTT GGA GAA AAG CTT GTC TTA AAT TGT ACA GCA AGA ACT GAA CTA AAT GTG GGG ATT
 AGA CAA CCT CTT TTC GAA CAG AAT TTA ACA TGT CGT TCT TGA CTT GAT TTA CAC CCC TAA
 S V G E K L V L N C T A R T E L N V G I>
 141 145 hFLK1 IG DOMAIN 3 155 160>

490 500 510 520 530 540
 * * * * * *

GAC TTC AAC TGG GAA TAC CCT TCT TCG AAG CAT CAG CAT AAG AAA CTT GTA AAC CGA GAC
 CTG AAG TTG ACC CTT ATG GGA AGA AGC TTC GTA GTC GTT GAA CAT TTG GCT CTG
 D F N W E Y P S S K H Q H K K L V N R D>
 161 165 hFLK1 IG DOMAIN 3 175 180>

550 560 570 580 590 600
 * * * * * *

CTA AAA ACC CAG TCT GGG AGT GAG ATG AAG AAA TTT TTG AGC ACC TTA ACT ATA GAT GGT
 GAT TTT TGG GTC AGA CCC TCA CTC TAC TTC TTT AAA AAC TCG TGG AAT TGA TAT CTA CCA
 L K T Q S G S E M K K F L S T L T I D G>
 181 185 hFLK1 IG DOMAIN 3 195 200>

610 620 630 640 650 660
 * * * * * *

GTA ACC CGG AGT GAC CAA GGA TTG TAC ACC TGT GCA GCA TCC AGT GGG CTG ATG ACC AAG
 CAT TGG GCC TCA CTG GTT CCT AAC ATG TGG ACA CGT CGT AGG TCA CCC GAC TAC TGG TTC
 V T R S D Q G L Y T C A A S S G L M T K>
 201 205 hFLK1 IG DOMAIN 3 215 220>

670 680 690 700 710 720
 * * * * * *

AAG AAC AGC ACA TTT GTC AGG GTC CAT GAA AAG GAC AAA ACT CAC ACA TGC CCA CCG TGC
 TTC TTG TCG TGT AAA CAG TCC CAG GTA CTT TTC CTG TTT TGA GTG TGT ACG GGT GGC ACG
 K N S T F V R V H E K>
 221 hFLK1 IG DOMAIN 3 231>

D	K	T	H	T	C	P	P	C>
232								240>

730 740 750 760 770 780
 * * * * * *

CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC
 GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG
 P A P E L L G G P S V F L F P P K P K D>
 241 245 hFCAC1 A 255 260>

790 800 810 820 830 840
 * * * * * *

ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA
 TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT
 T L M I S R T P E V T C V V V D V S H E>
 261 265 hFCAC1 A 275 280>

850 860 870 880 890 900
 * * * * * *

GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA
 CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA TTA CGG TTC TGT
 D P E V K F N W Y V D G V E V H N A K T>
 281 285 hFCAC1 A 295 300>

Figure 24C

910 920 930 940 950 960
 * * * * * *
 AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG
 TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC
 K P R E E Q Y N S T Y R V V S V L T V L>
 301 305 hFCAC1 A 315 320>

970 980 990 1000 1010 1020
 * * * * * *
 CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA
 GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG CAG AGG TTG TTT CGG GAG GGT
 H Q D W L N G K E Y K C K V S N K A L P>
 321 325 hFCAC1 A 335 340>

1030 1040 1050 1060 1070 1080
 * * * * * *
 GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC
 CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG
 A P I E K T I S K A K G Q P R E P Q V Y>
 341 345 hFCAC1 A 355 360>

1090 1100 1110 1120 1130 1140
 * * * * * *
 ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC
 TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG
 T L P P S R D E L T K N Q V S L T C L V>
 361 365 hFCAC1 A 375 380>

1150 1160 1170 1180 1190 1200
 * * * * * *
 AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC
 TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG
 K G F Y P S D I A V E W E S N G Q P E N>
 381 385 hFCAC1 A 395 400>

1210 1220 1230 1240 1250 1260
 * * * * * *
 AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TIC TTC CTC TAC AGC AAG
 TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC
 N Y K T T P P V L D S D G S F F L Y S K>
 401 405 hFCAC1 A 415 420>

1270 1280 1290 1300 1310 1320
 * * * * * *
 CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT
 GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA
 L T V D K S R W Q Q G N V F S C S V M H>
 421 425 hFCAC1 A 435 440>

1330 1340 1350 1360 1370
 * * * * *
 GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
 CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT
 E A L H N H Y T Q K S L S L S P G K *>
 441 445 hFCAC1 A 455 458 >

Figure 25B

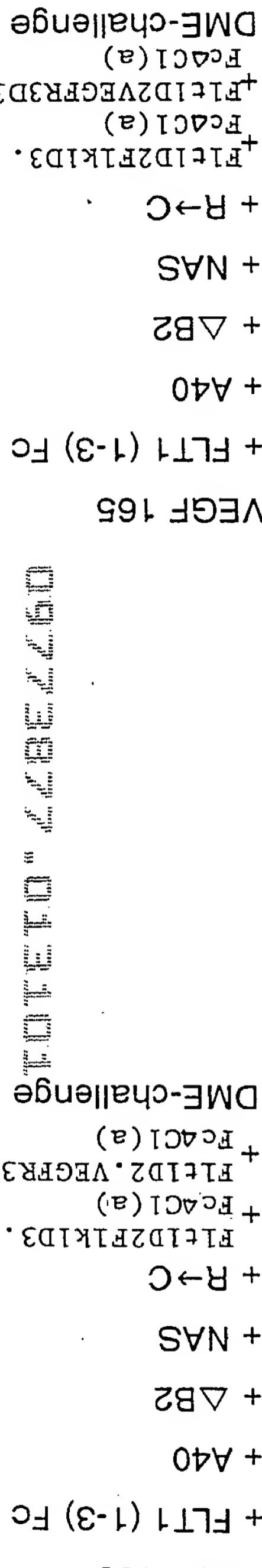
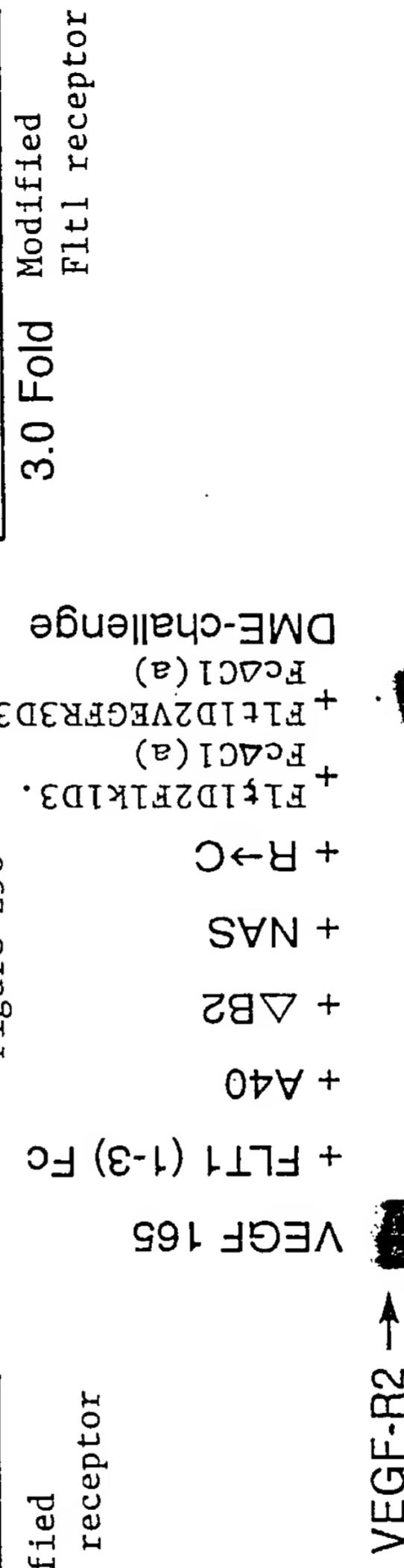


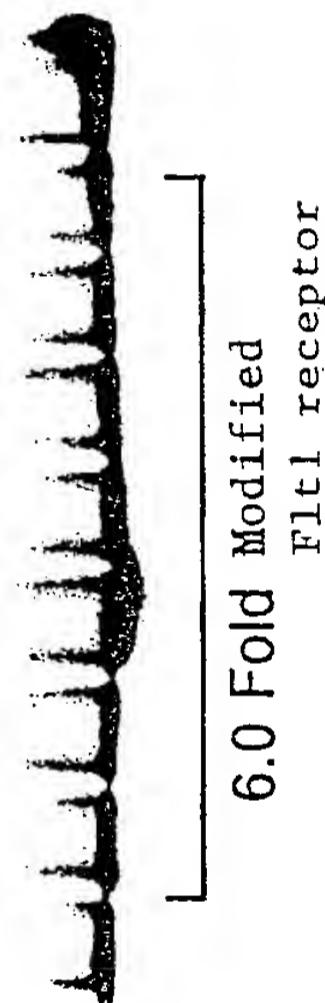
Figure 25A



Figure 25C



3.0 Fold Modified Flt1 receptor



6.0 Fold Modified Flt1 receptor

Figure 26B

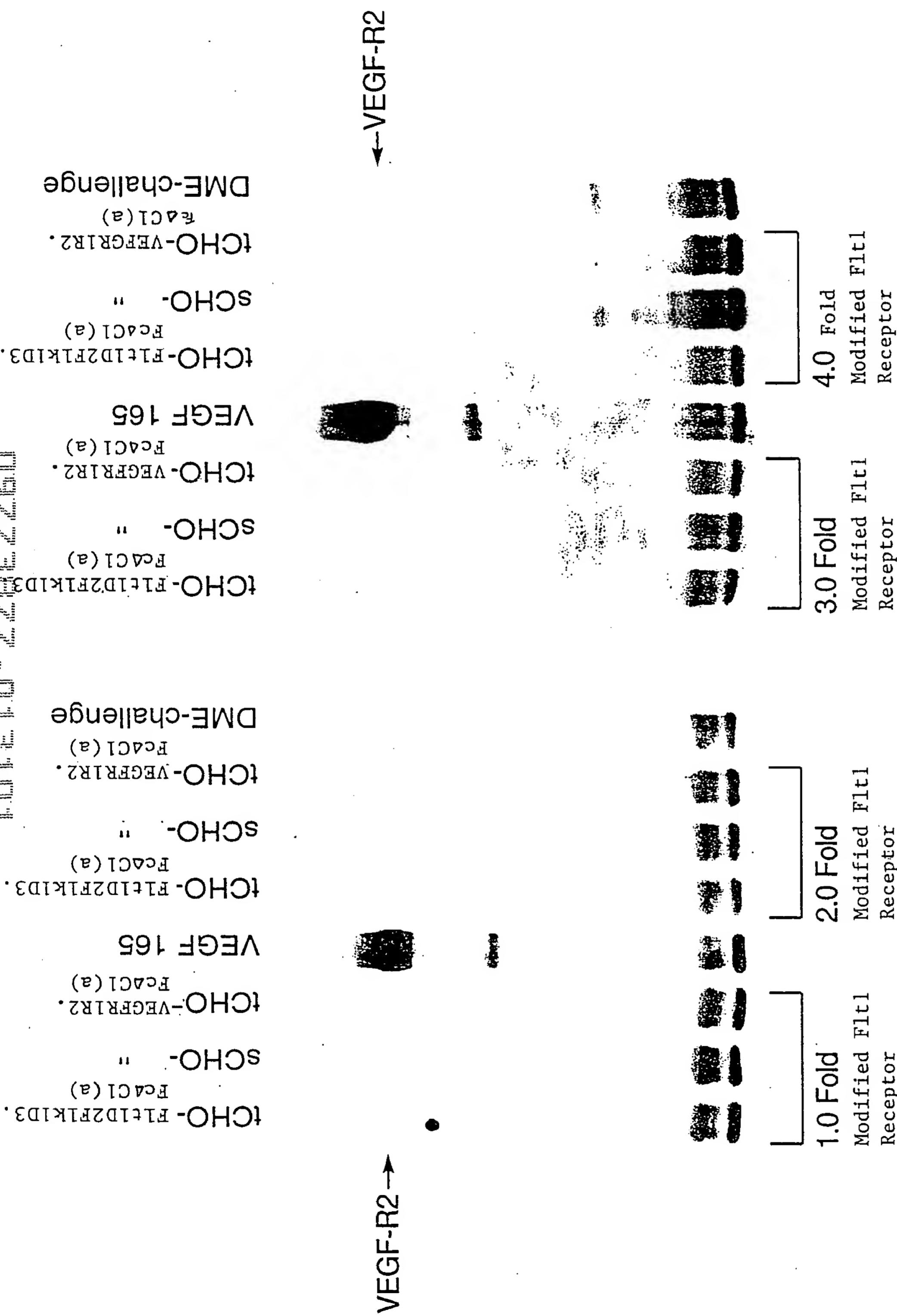


Figure 26A

Figure 27

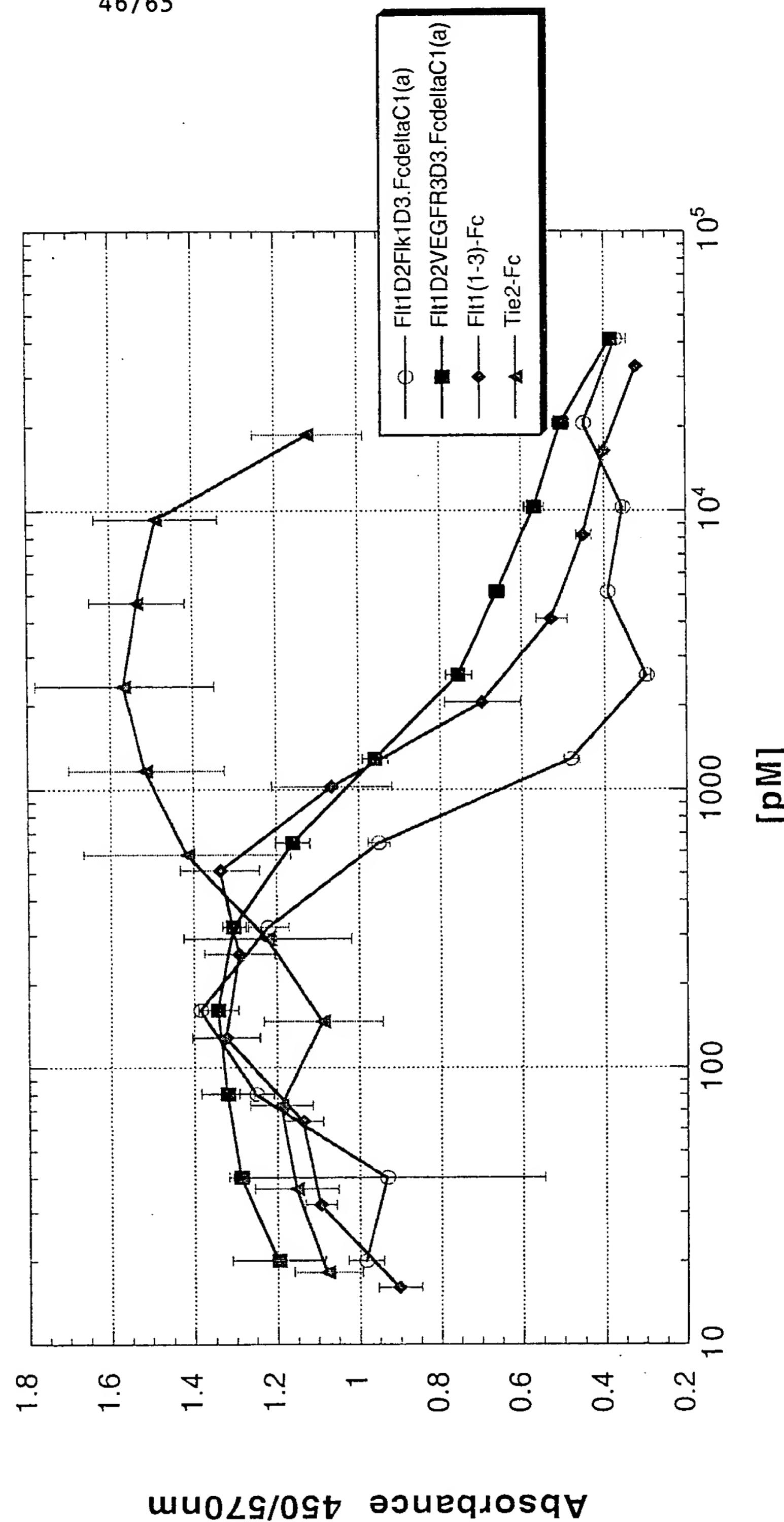


Figure 28

<u>Binding Stoichiometry of hVEGF165 to F1t1D2F1k1D3.FcΔC1(a) & VEGFR1R2-FcΔC1(a)</u>		
<u>hVEGF165 (nM)</u>	<u>VEGF/F1t1D2F1k1D3.FcΔC1(a)</u>	<u>VEGF/VEGFR1R2-FcΔC1(a)</u>
1	0.93	0.98
10	0.97	0.94
50	1	0.99
Average±StDev	0.96±0.03	0.97±0.02

Figure 29

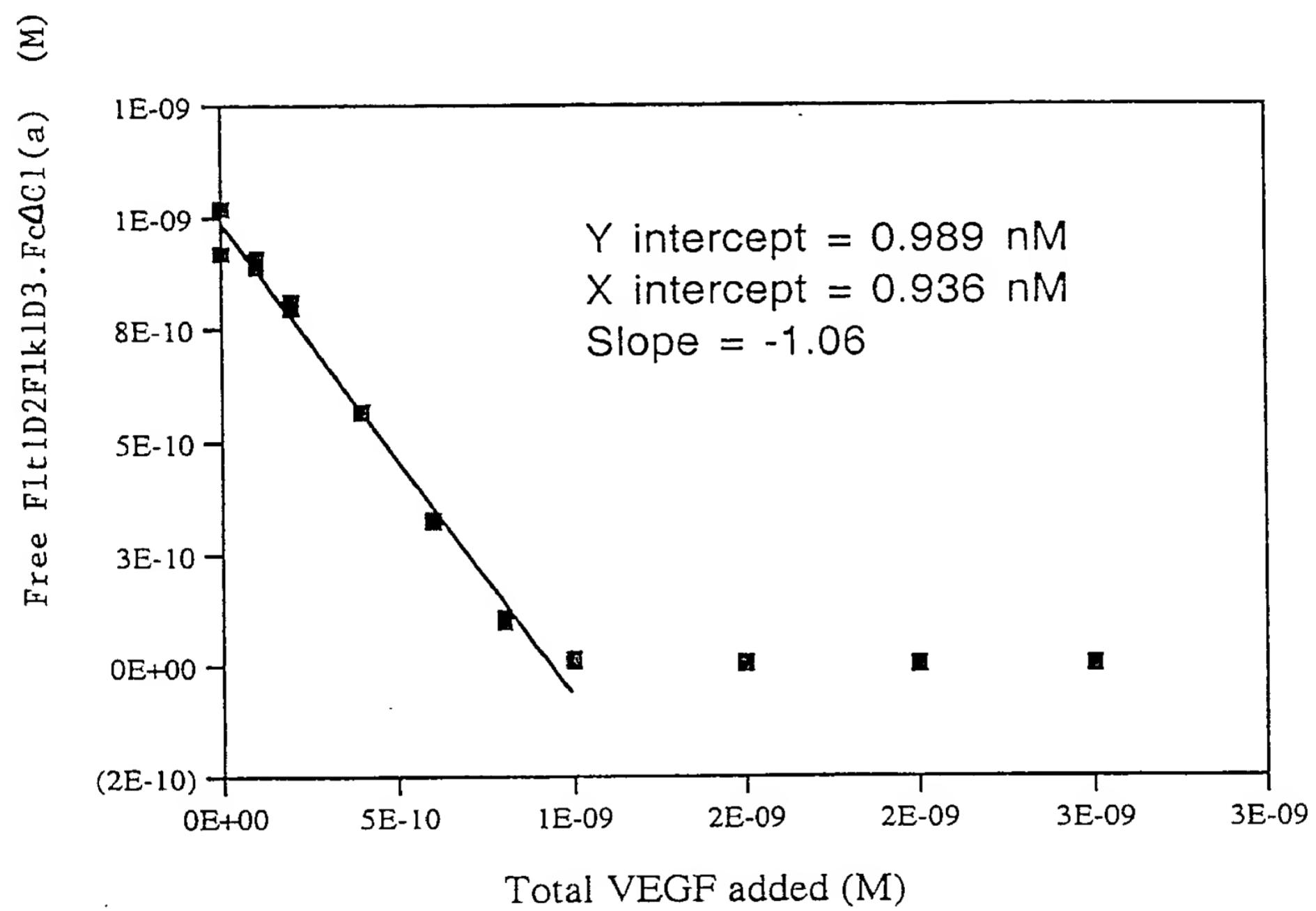


Figure 30

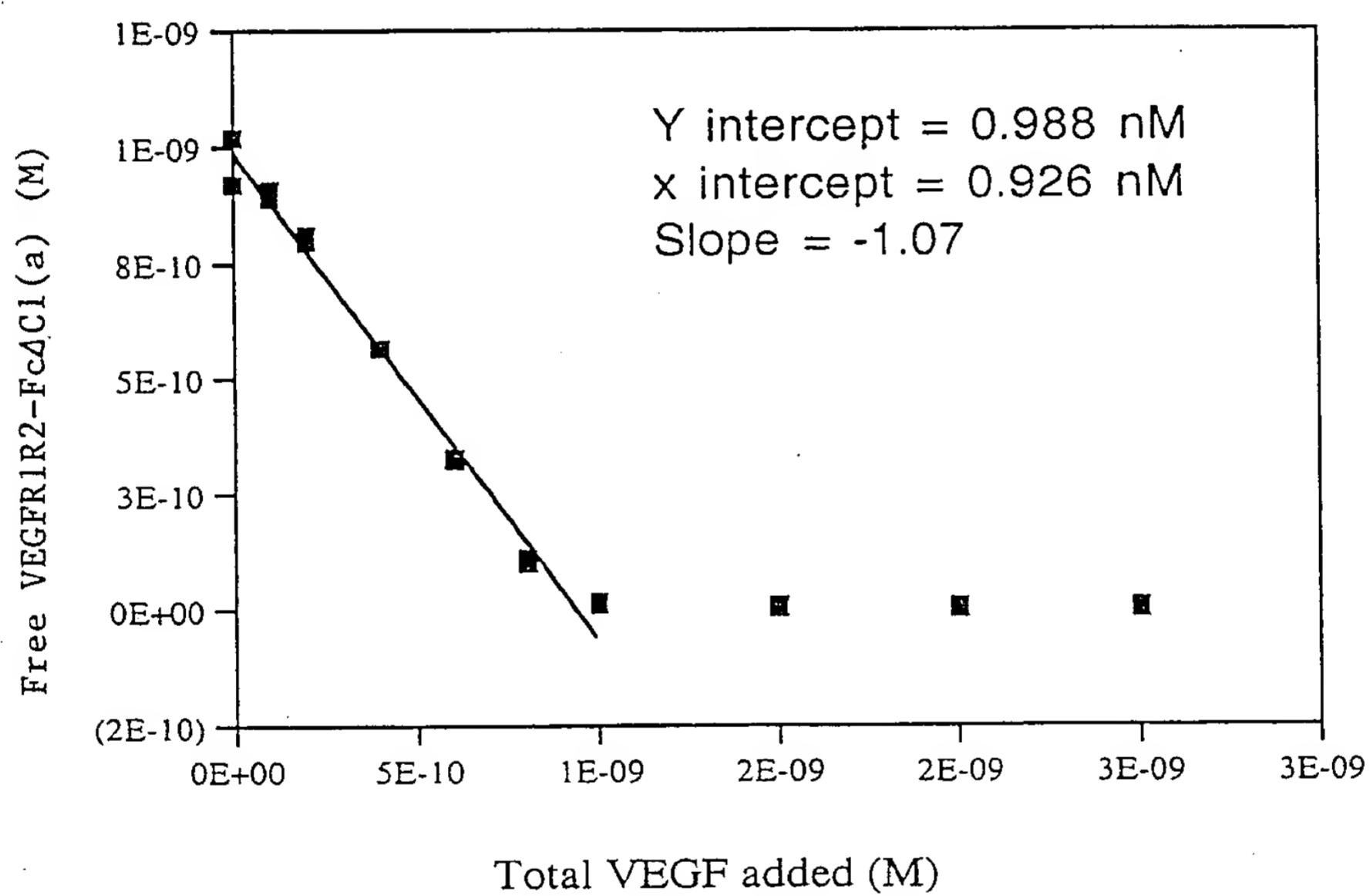


Figure 31

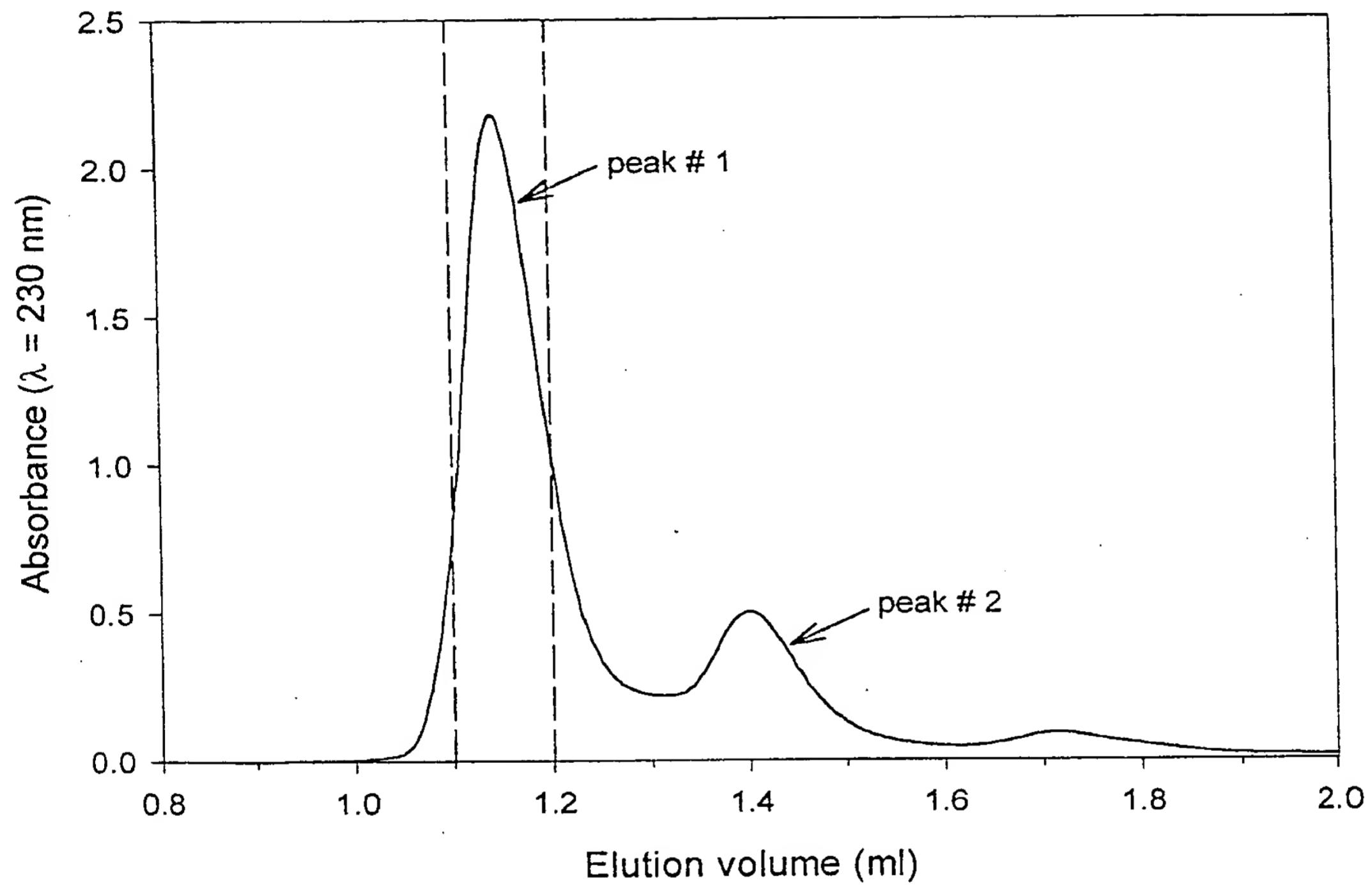


Figure 32

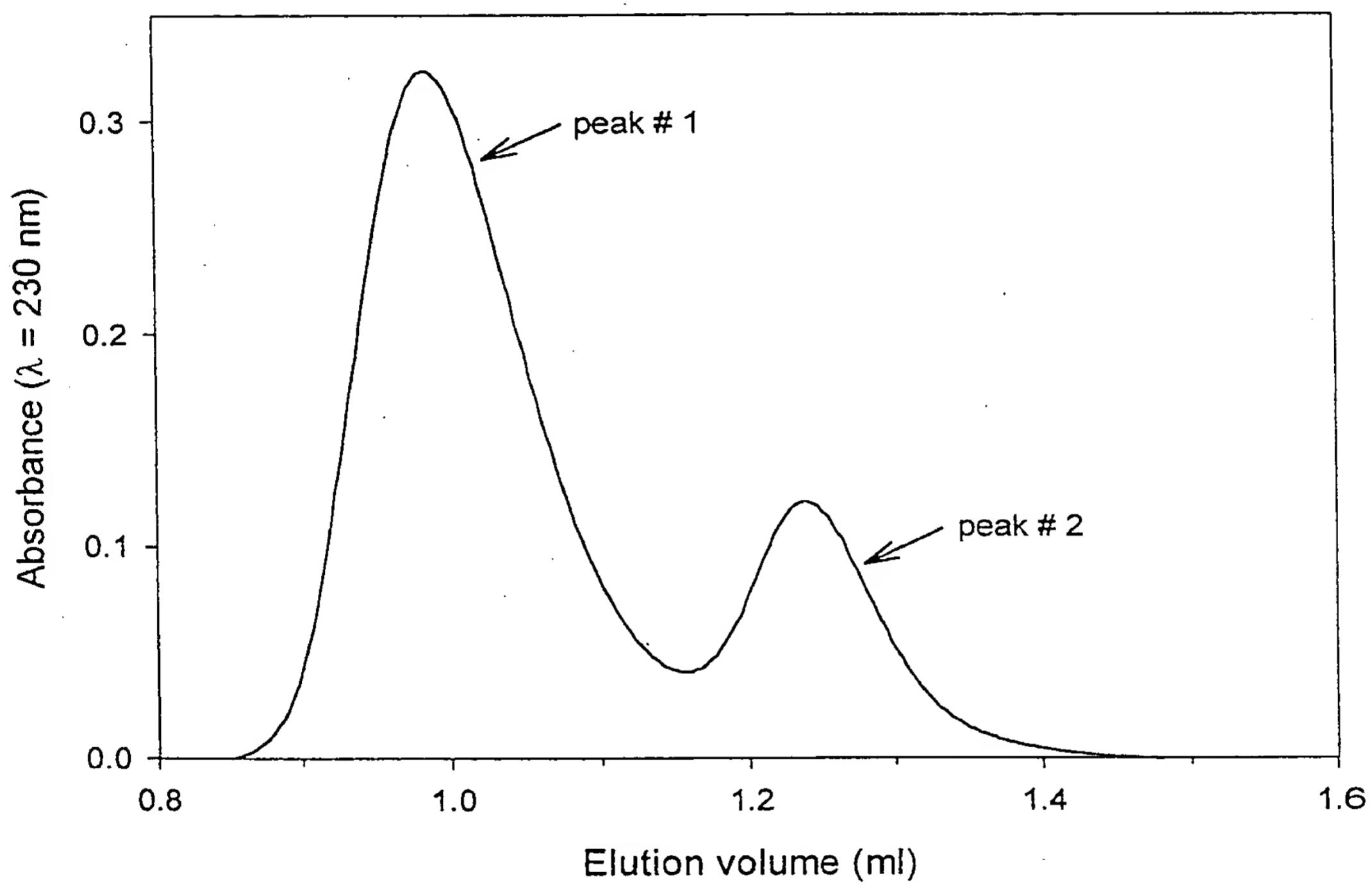


Figure 33

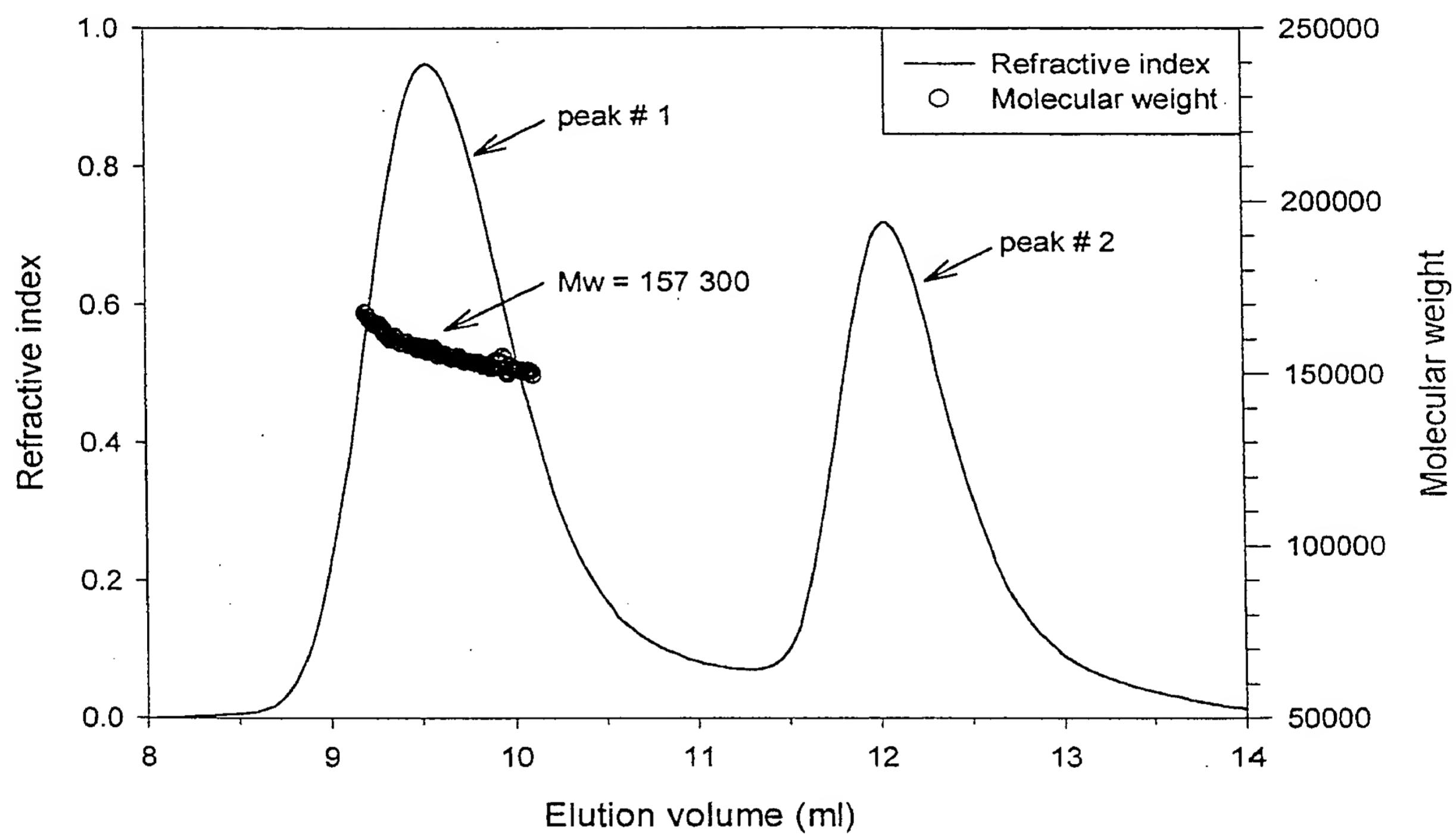


Figure 34

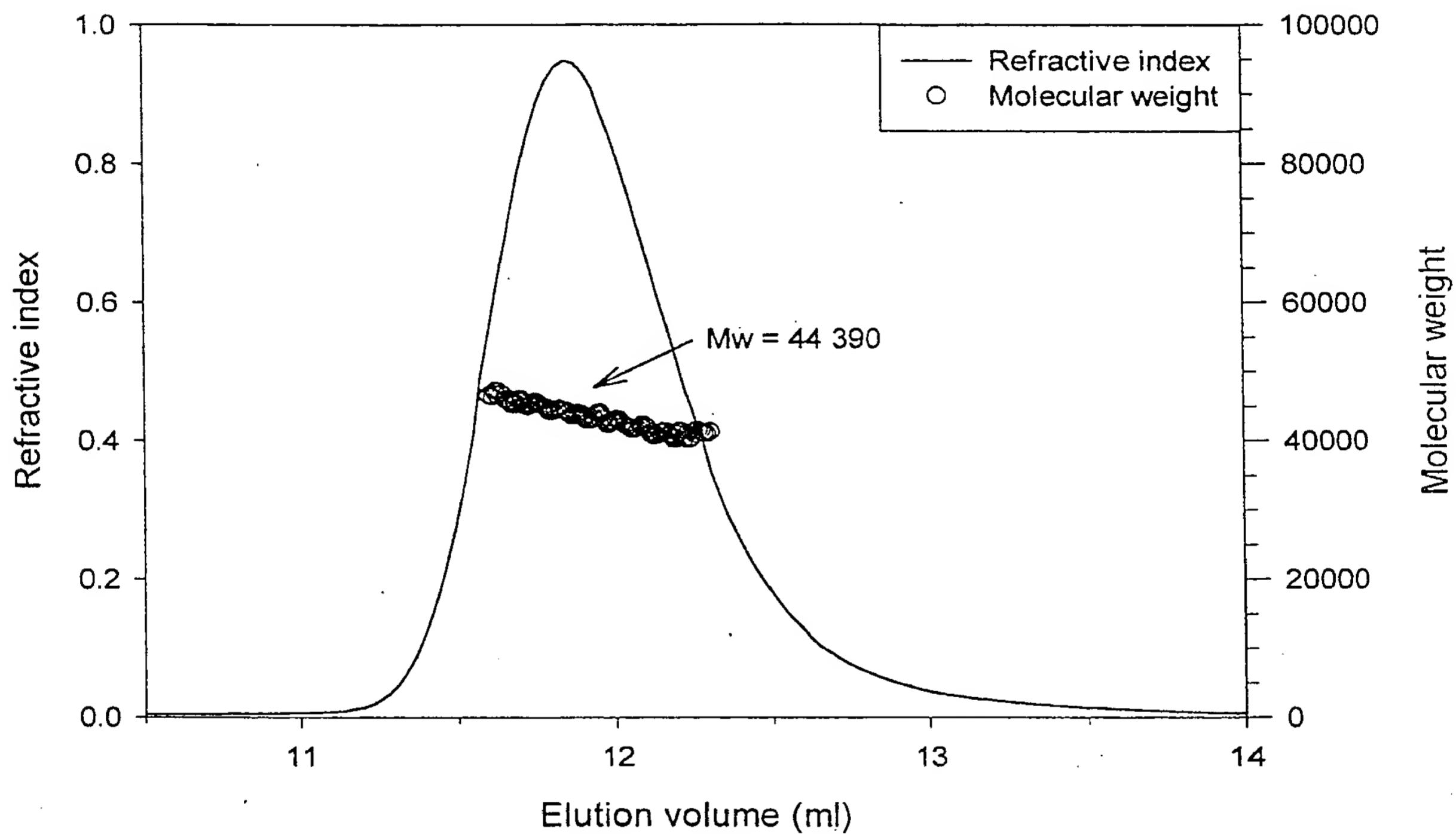


Figure 35

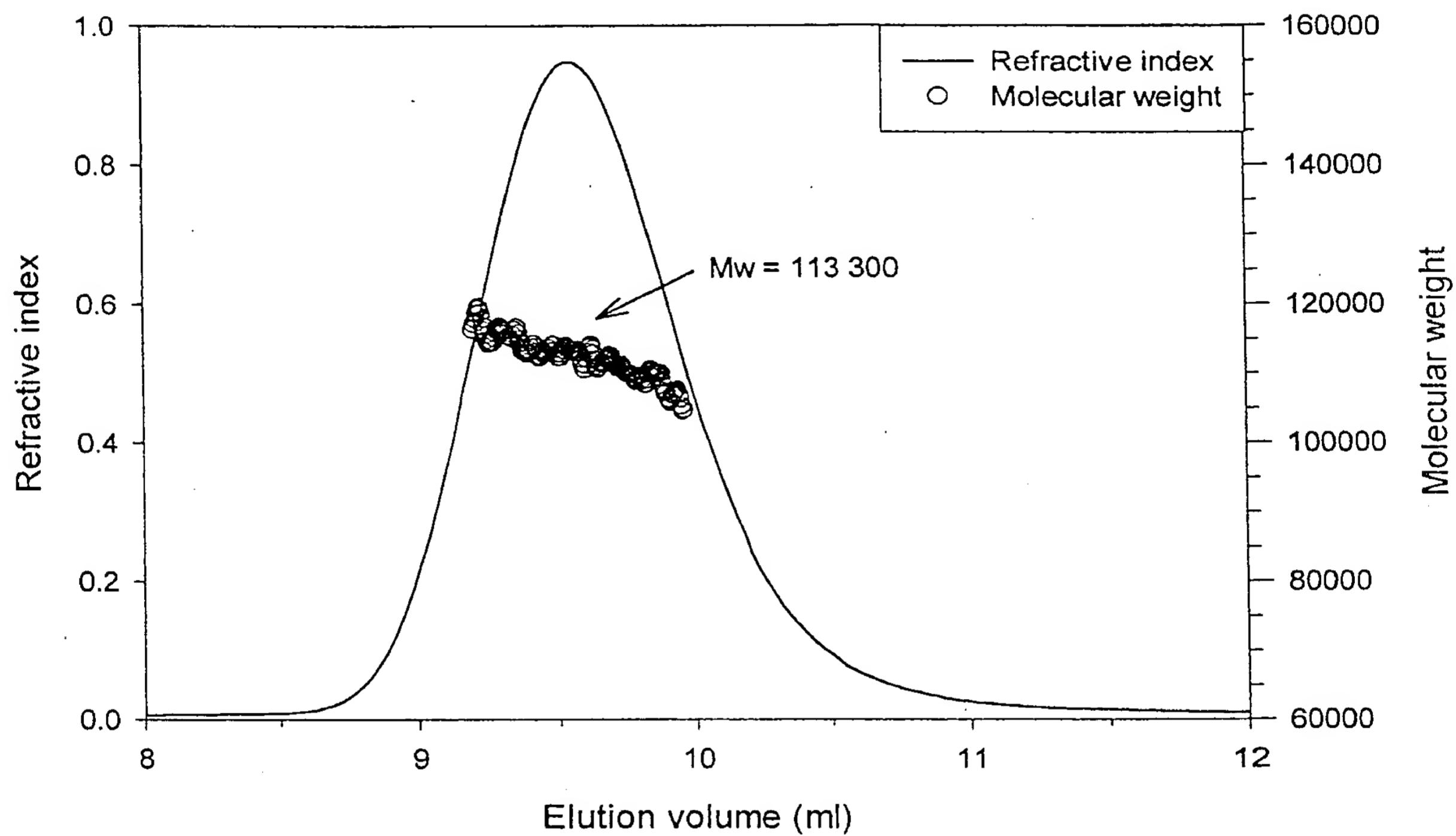


Figure 36

GRPFVEMYSEIPEIHMTEGRELVIPCRVVTSPNITVTLKKFPLDTLIPDG
50
R
KRIWDSRKGFISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTID
100

VVLSPSHGIELSVEKLVLNCTARTTELNVGIDFNWEYPSSKHQHKKLVNR
150

DLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVVRVH
200

EKGP GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
250
I
C
X
I
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTLHQDWLN
300

GKEYKCKVSNKALPAEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
350

TCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS
400

RWQQGNVFSCSVMHEALHNHYTQKSLSISPGK
450

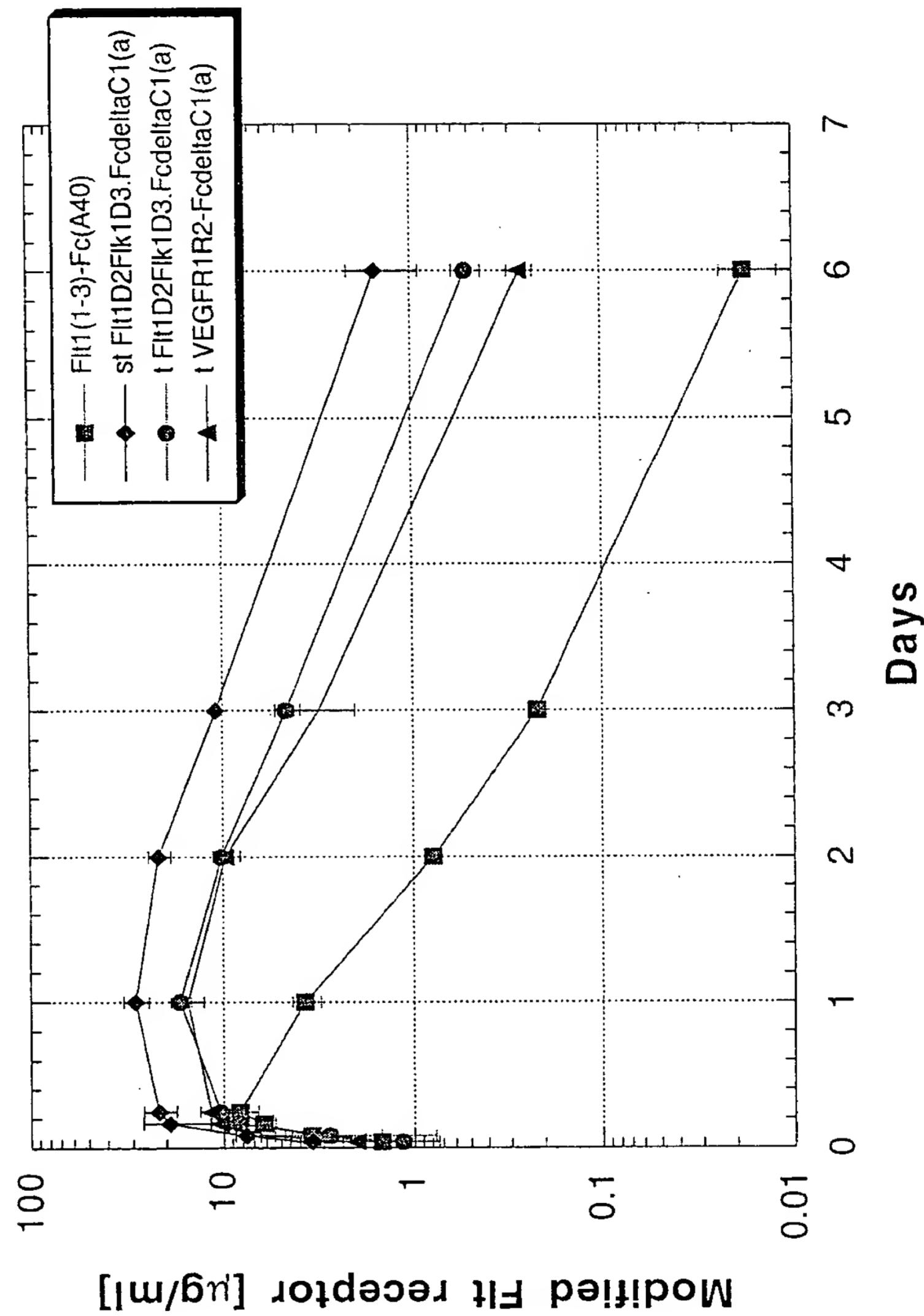
Figure 37

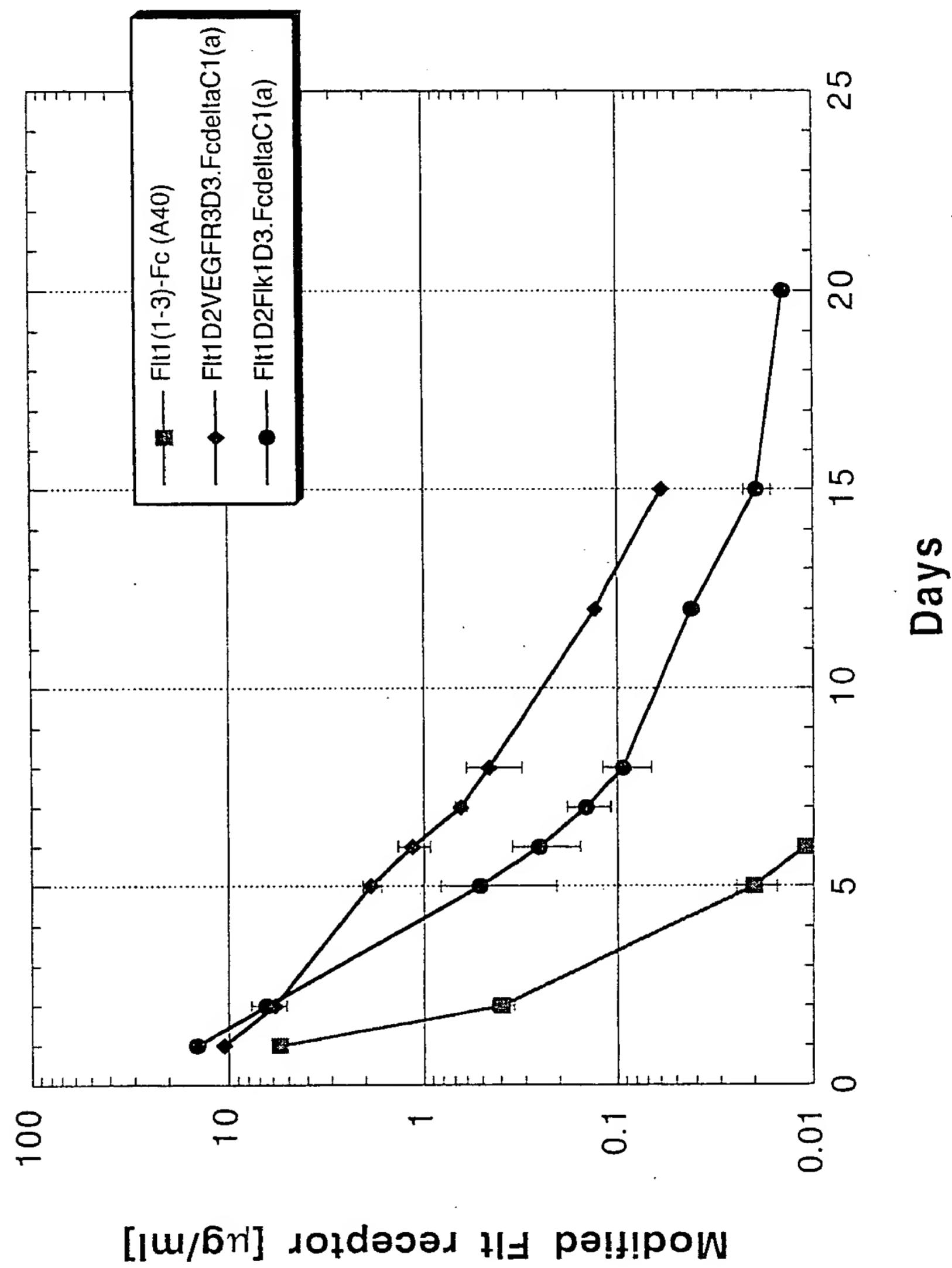
Figure 38

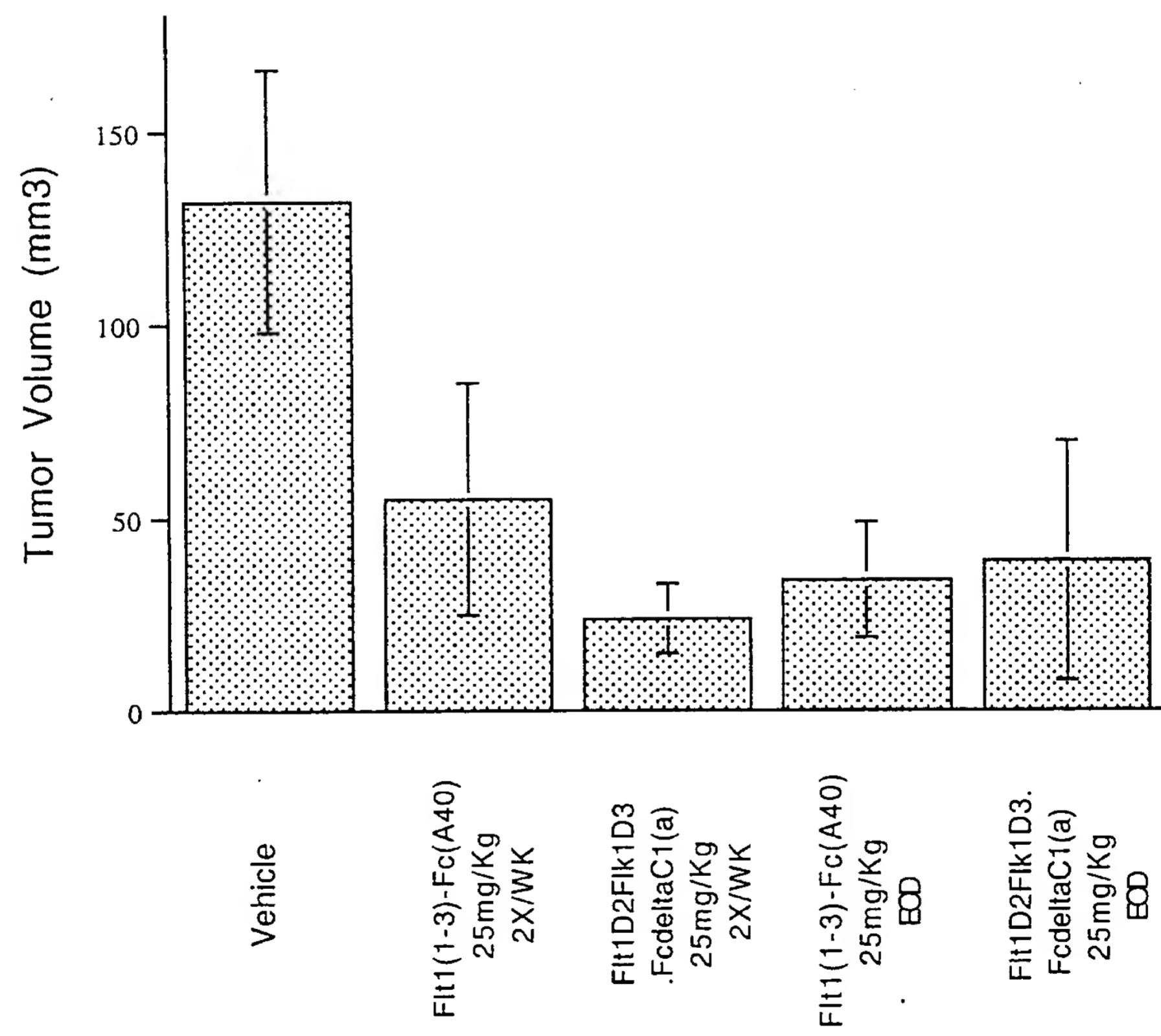
Figure 39

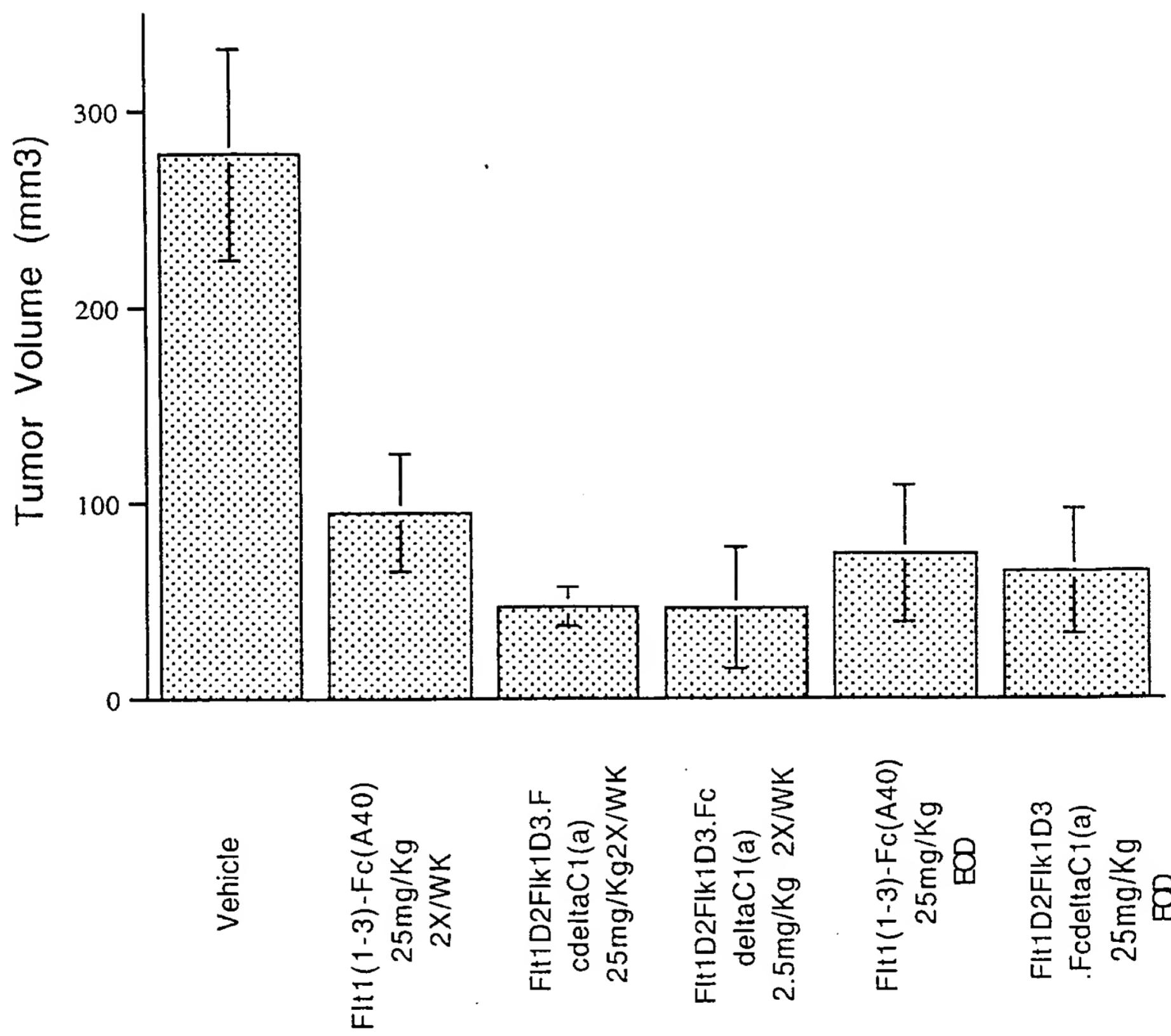
Figure 40

Figure 41

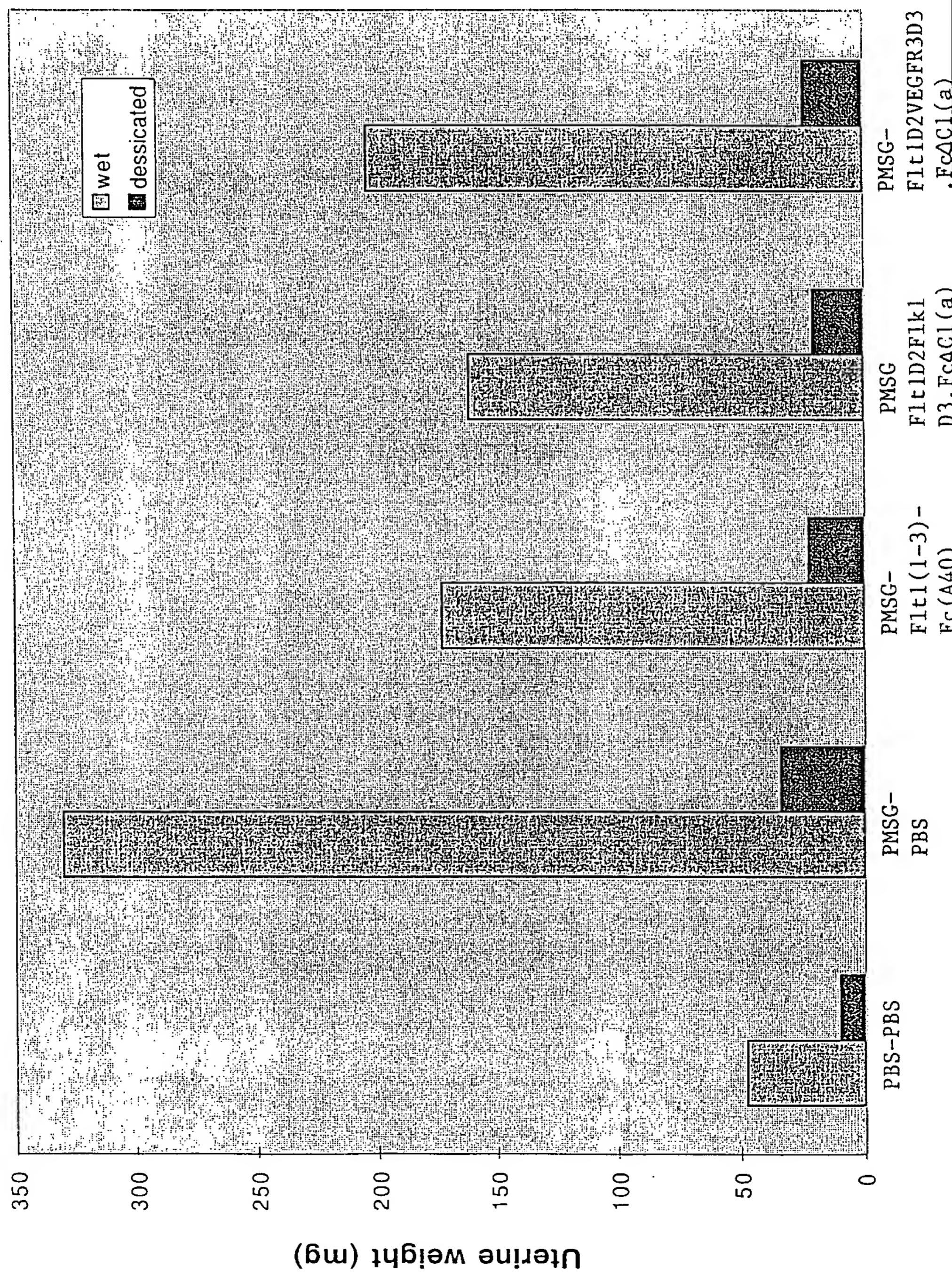


Figure 42A

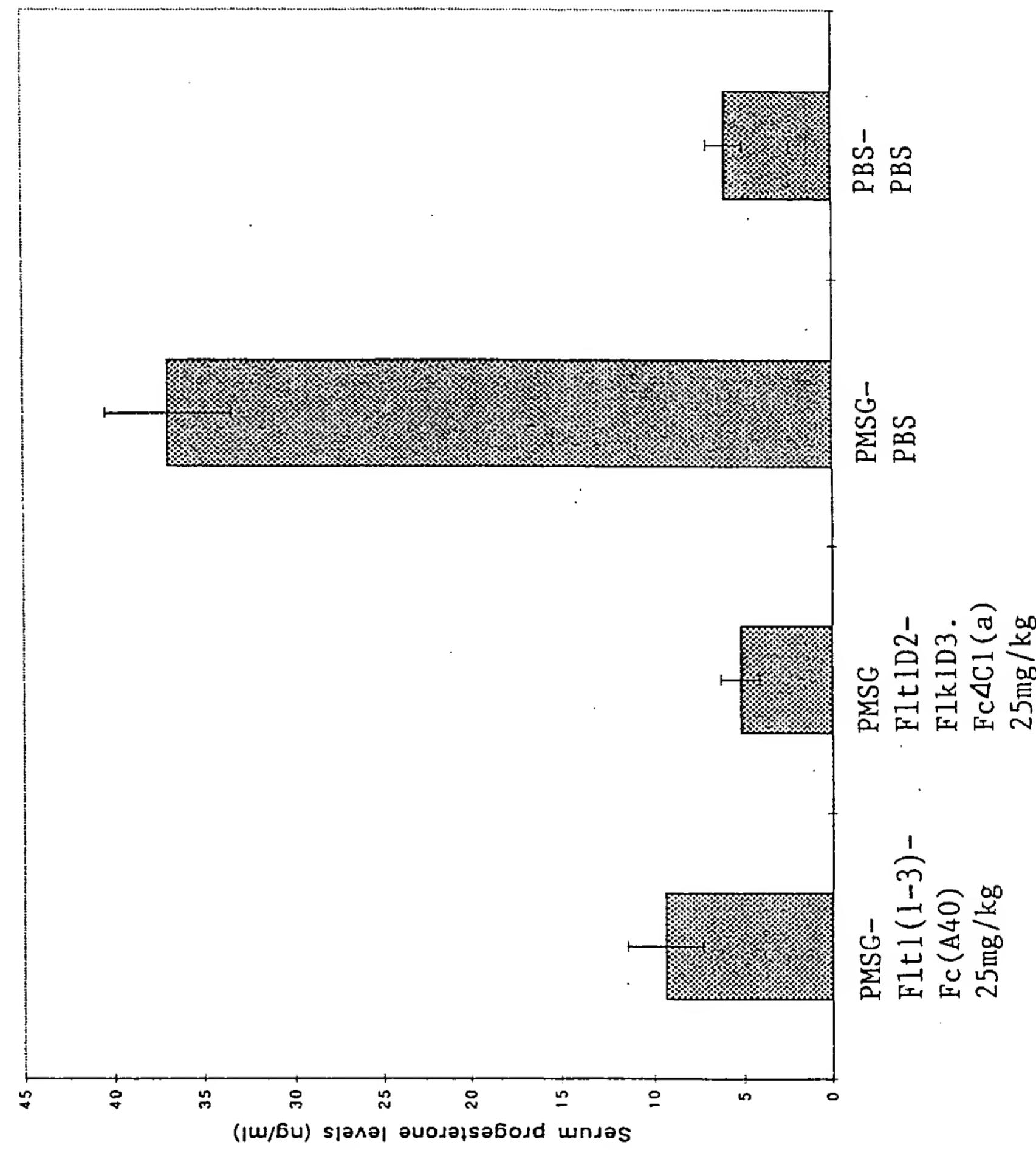


Figure 42B

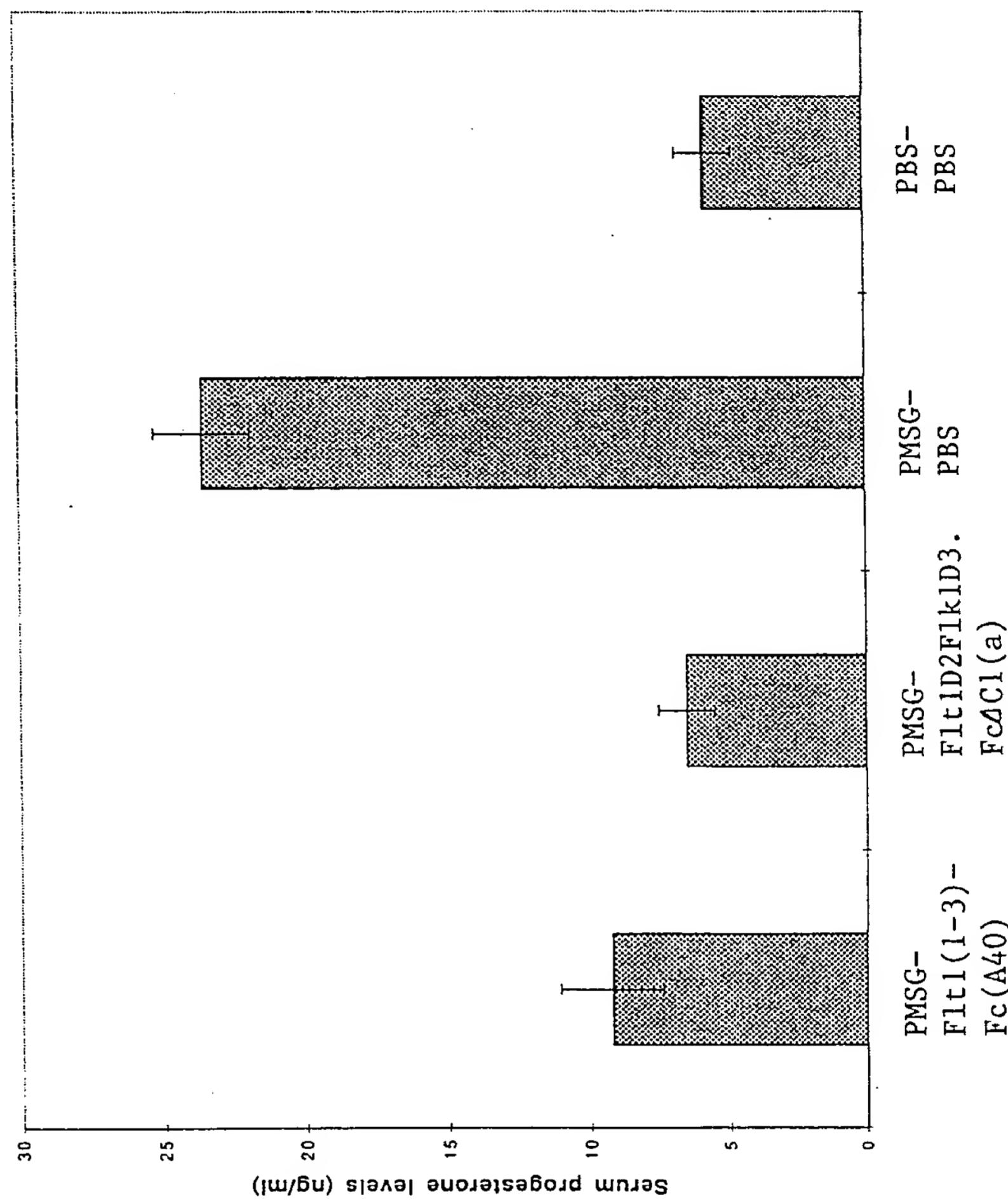


Fig.43



Fig.44 A-C

Fig.44A

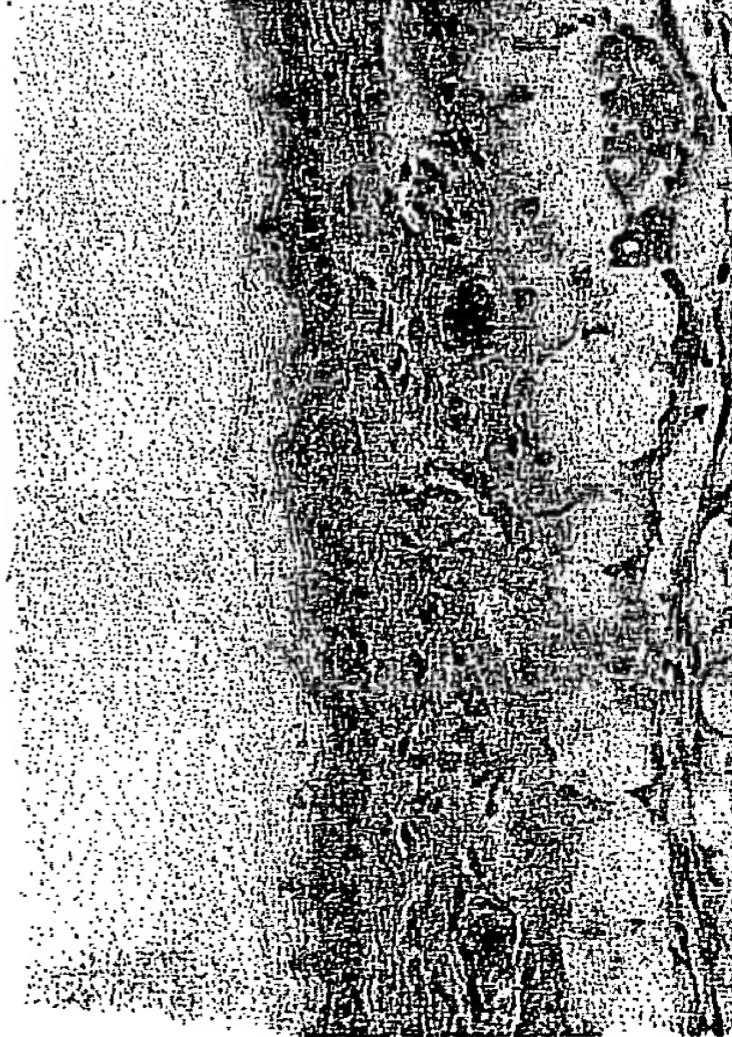


Fig.44B

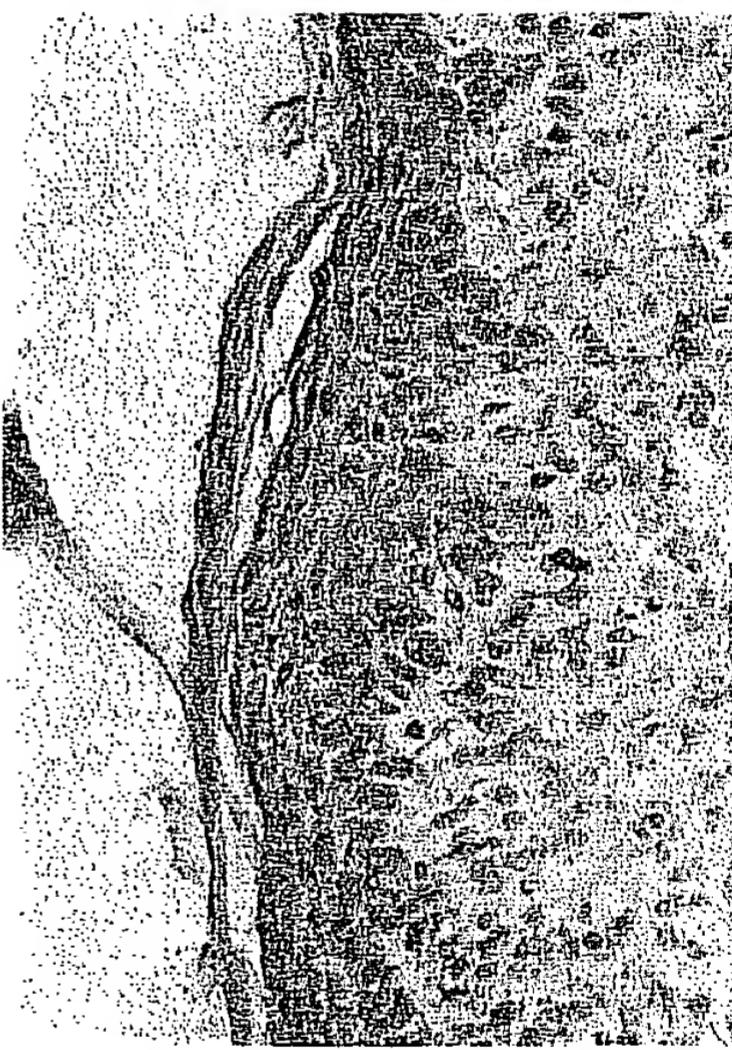


Fig.44C

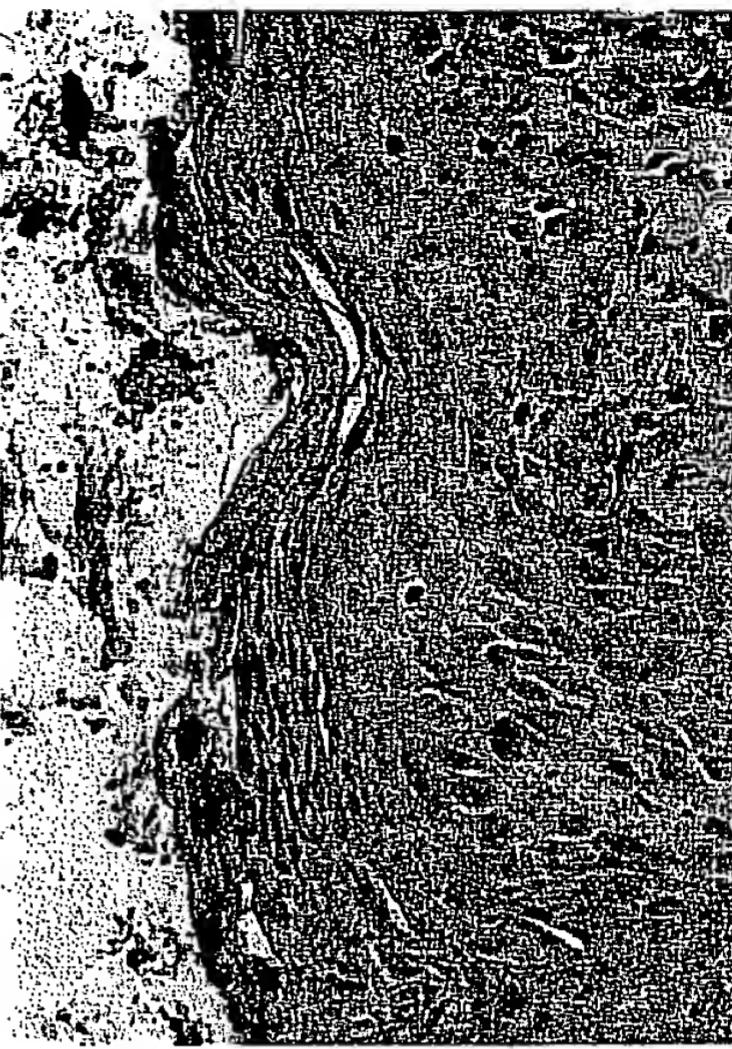


Fig.45



Fig.46 A-B

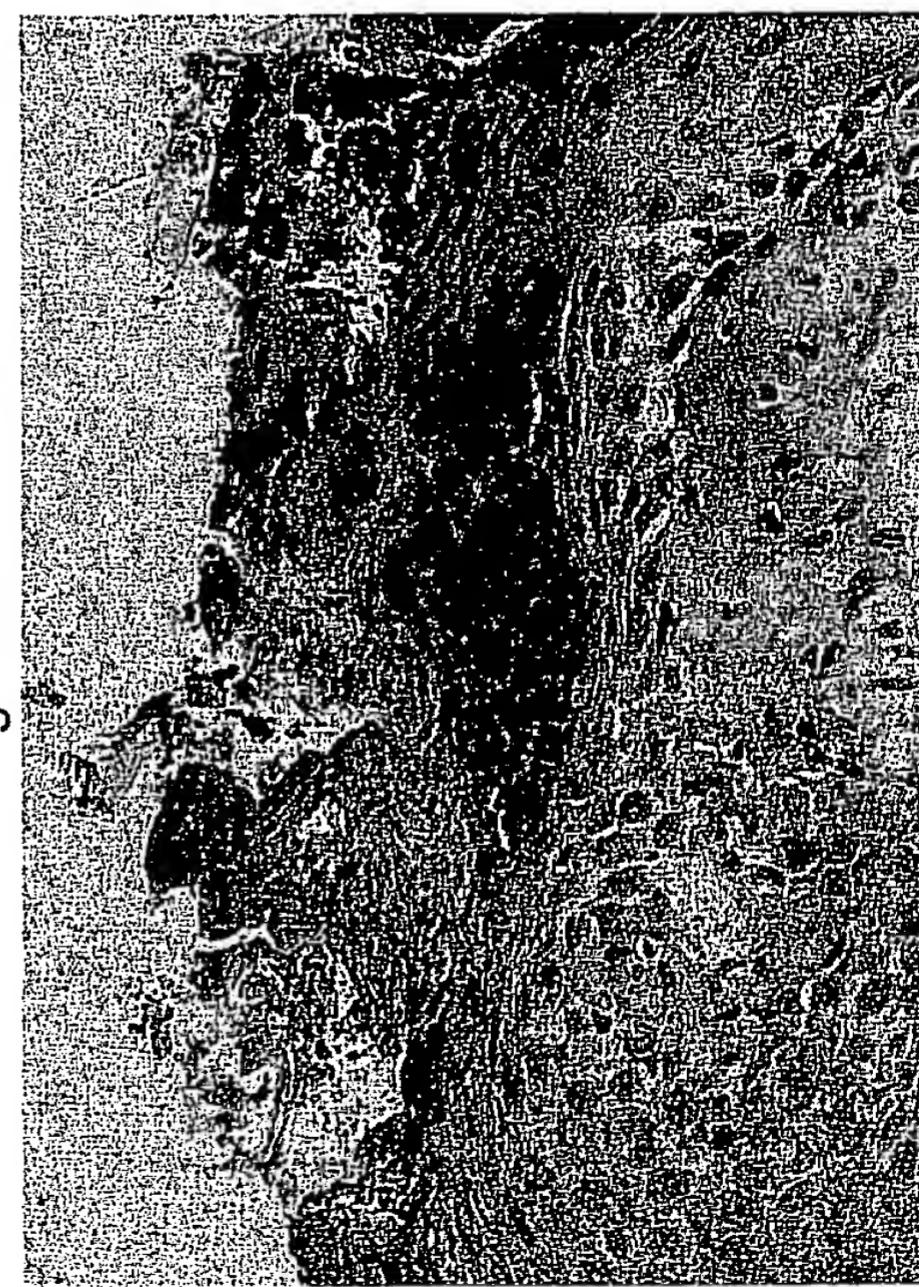


Fig.46B



